

601-1-098CIP

		I		II	
human EF2K	122	GEWLDDVLKMASQPFGRGAMRECFRTKKLSNFLHAQ	-----	QWKGASNYVAKRYIEPVD	-----
C. e. EF2K	108	KQWTEIDVDVRLHPDSFARGAMRECYRLKKCSKHGTSQ	-----	DW--SSNYVAKRYICQVD	-----
MHCK A	570	NKWIRLSMKLKVERKPPFAEGALREAYHTVSLGVGTDENYPLGTTTKJLFPPIEMISPISKNNEAMTQLKNGTKFVLKLYKKEAE	-----	SGRYVSKIGKK--	-----
MHCK B	130	AQWTCATLVKVEPVPPFAEGAFRKAYHTLDLSKSGA	-----	DQGLVGKFSFNKK--	-----
FC-AN09	1	IVCVSIEKTPFAKGSCTAHKCLKDWSQP	-----	*****OVK*****	-----
consensus		***W*****O*O*****F**G**R**O*****			
		III		IV	
human EF2K	178	---RDVYFEDVRLQMEAKLWGEENRHHKPPKQVDIMQMCIELKDR---	PGKPLF-HLEHYIEGKYIKYNSNSGFVRDDNI		
C. e. EF2K	162	---RRVLFDDVRLQMDAKLWAEENRYNPPKKIDIVQMCVIEIDV---	KGSPLY-HLEHFIEGKYIKYNSNSGFVSNA--		
MHCK A	653	QASRELYFEDVKMQMVCRDWGNKFNQKKPPKKIEFLMSWVVELIDRSPSSNGQPILCSIEPLLVGEFKKNSNYGAVLTN--			
MHCK B	177	-PTPRPSYFEDVKMQMIAKKWADKYNSEFKPPKKIEFLQSCVLEFVDRTSSD---	LICGAEPYVEGQYRKYNNSNGFVSND--		
FC-AN09	42	--TTRDSYFTDVLMTFCAKWAEKFNKAKPPKPIITFLPSYVYELIDHPPPY---	PV-CGGEPEFIEGDYKHHNNNSGYVSSDA--		
consensus		***R**OF*DV*OQ*****W*****ON**PPK*O*O*****E*O*O*G*O*K*N*N*G*V*****			
		V		VI	
human EF2K	252	RLTPQAFSHFTFERSGHQLIVVDIQGVGDLYTDPQIHTETGTDFGDNLGVRGMALEFFYSHACNRICESMGLAPFDLSPRERD			
C. e. EF2K	235	RLTPQAFSHFTFERSGHQMMVVDIQGVGDLYTDPQIHTVVGTDYGDNLGTRGMALFFHSHRCNDICETMDLSNFELSPPELE			
MHCK A	734	RSTPQAFSHFTYELSNKQMIVVDIQGVDDLYTDPQIHTPDGKGFGGLGNLKGAGINKFIITHKCNACALLDL-DVKLG----			
MHCK B	254	RNTPQSFHFTYEHSHNHQLLIIDIQGVGDHYTDPQIHTYDGVGFGIGNLGQKGFELDTHKCNACIQQYINLQSN-----			
FC-AN09	118	RNTPQSFHFSYELSNHHELLIVDIQGVNDFYTDPQIHTKSGEGFEGNLGETGFHKFLQTHKCNPVCDLKLKPIN-----			
consensus		R+TPQ+FSHF*OE*S**+O*O*O*DIQGV*DOYTDPQIHT**G**OG*GNLG**GO**H*CN*OC**O*L**O*****			
		VII			
human EF2K	335	AVNQNTKLLQSAKT--ILRGTEEEKCGS			
C. e. EF2K	318	ATEVAMEVAQKQKSCIVPPPVFEARR			
MHCK A	811	-----GVLSGNNKKQ--LQQGTMVMPDI			
MHCK B	330	-----PKSEKSDC---GTVPRPDL			
FC-AN09	194	-----QSKKA--LLRGTLPVVQL			
consensus		*****K*****T*****			

Figure 1A

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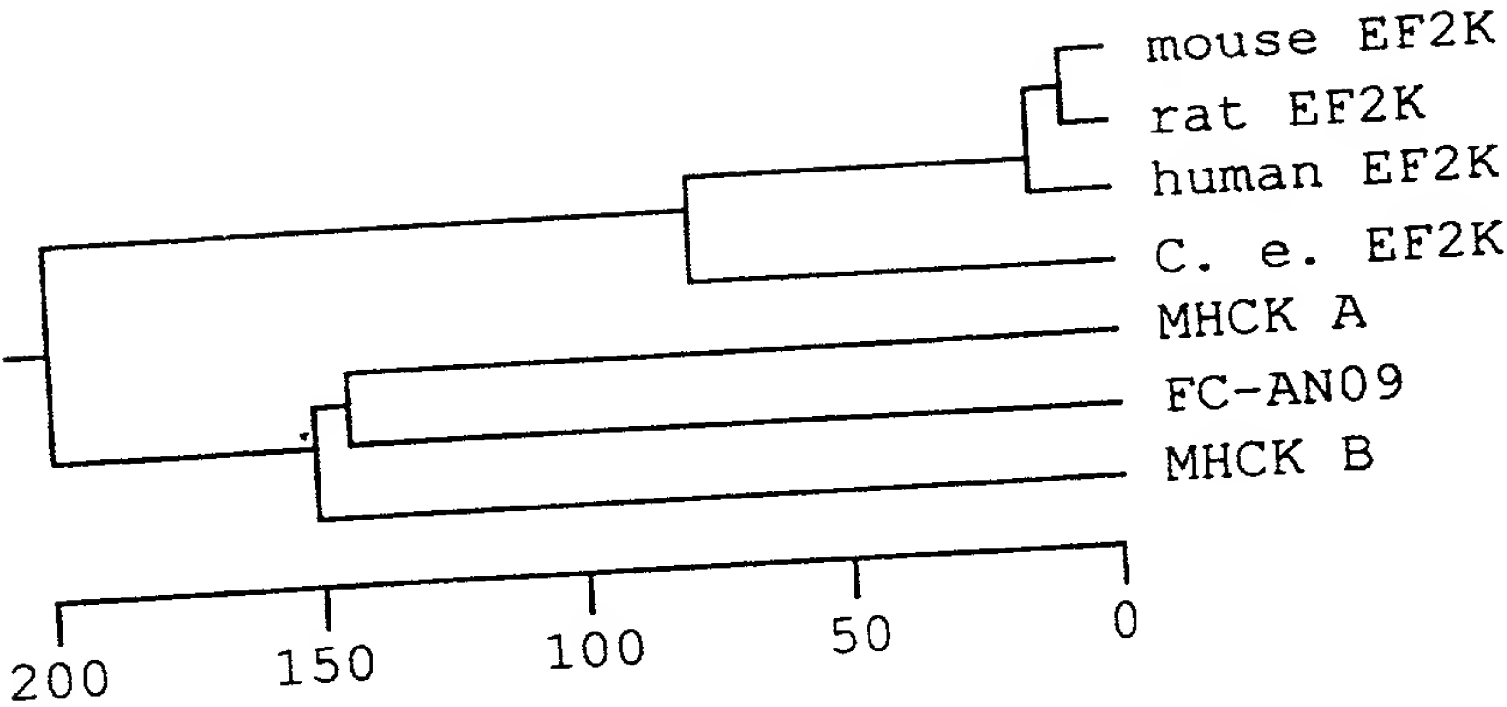


Figure 1B

601-1-098CIP

human eEF-2K	1R.....QSP.....DG.....G.....E.....	44
C. elegans eEF-2K	1	MTIDTTNESDNTSPGLEASARTFSLNASKMVR-----ITD	38
mouse eEF-2K	1	MAEDLIFCLEGVGGRCRAAGHNADSDTDSDDDEGYFICPITD	44
human eEF-2K	45	.PS.....N.....NK.....S.RY.SS.....N.....Q.....	93
C. elegans eEF-2K	39	DYADEVFIEQNDDVIEKPRMD-----PLHVRKLMEIWRKAARRART	79
mouse eEF-2K	45	DHMSNQNVSSKVQSYSNLTKTECGS-TGSPASSFHFKEAWKHAEKAK-	92
human eEF-2K	94R.....D.....	143
C. elegans eEF-2K	80	NYIDPWDEENIHEYPVQRAKRYRYSAIRKQWTEIIVDVRIHPDSFARGAM	129
mouse eEF-2K	93	HMPDPWAEFHLEDIATEHATHRYNAVGTGEWLKDEVLIKMASQPEGRGAM	142
MHCK A	572	WIRLSMKLVKVERKPEAECAI	591
human eEF-2K	144RECYRLKKCS-----KHGTSQDW--SSN	166
C. elegans eEF-2K	130	RECERTKKLS-----NFLHAQQWKGASN	165
mouse eEF-2K	143	REAYHTVSLGVGTDENYPLGTTKLFPPIEMISPISKNNNEAMTQLKNGIK	641
MHCK A	592D.....R.....E.....	212
human eEF-2K	167	YVAKRYICQVD-----RRVLFDDVRLQMDAKLWAEENRYNRPKKIDIVQM	196
C. elegans eEF-2K	151	YVAKRYIEPVD-----RSVYFEDVQLQMEAKLWGEDYNRHKPPKQVDIMQM	211
mouse eEF-2K	166	EVLKLYKKEAEQQASRELIFEDVKMQMVCRDWGNKENQKKPPKKIEFLMS	691
MHCK A	642K.....	256
human eEF-2K	213	CVIEMIDVK-----GSP-LYHLEHIEGKYIKYNSNSGFEV-S-NAAARLTPQ	239
C. elegans eEF-2K	197	CIELKDRP-----GQP-LFHLEHYIEGKYIKYNSNSGFEVRDDNI-RLTPQ	255
mouse eEF-2K	212	WVVELIDRSPSSNGQPIELCSLEPLVGEFEKKNNSNYGAVILT-N--RSTPQ	738
MHCK A	692		

Figure 2A

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human	eEF-2K	257T.....	306
C.elegans	eEF-2K	240	AFSHFTFERSGHQMVVVDIQGVGDLYTDPQIHTVVGTDYGDGNLGTGRGMA	289
mouse	eEF-2K	256	AFSHFTFERSGHQIIVVDIQGVGDLYTDPQIHTKEKGTDFGDGNLGVRGMA	305
	MHCK A	739	AFSHFTYELSNKQMIVVVDIQGVDDLYTDPQIHTPDGKGFGLGNLGKAGIN	788
human	eEF-2K	307E.....A.....R.....N.K.....	354
C.elegans	eEF-2K	290	LEFHSHRCNDICEETMDLSNFEFLSPPEIEATEVAMEVAAKQKKSCIVPPPTV	339
mouse	eEF-2K	306	LEFYSHACNRICQSMGLTTFEDLSPREQDAVNQSTRLLQSAKT--ILRGTE	353
	MHCK A	789	KEFITTHKCNACALIDL	805
human	eEF-2K	355V...G...-RP.....	400
C.elegans	eEF-2K	340	FEARRNRISSECVHVEHGISMDOQLRKRLTL--NQSSDLSAKSHNEDCV	386
mouse	eEF-2K	354	EKCGSPRIRTLSSS---RPPLL-LRLSENSGDENMSDVTFDLSLPSSPSA	399
human	eEF-2K	401S.....AS.....HL.....E.....	449
C.elegans	eEF-2K	387	CPECIPVVEQLCEPCSEDEEEDDYPRSEKSGNSQKSRSRMSISTRSS	436
mouse	eEF-2K	400	TPHSQKLDH-LHWPVFGDLDNMGPRDHRMDNHRDSENSGDSGYPSEKRS	448
human	eEF-2K	450	-E.....YS...-KY.....K.....S...	494
C.elegans	eEF-2K	437	GDESASRPRKCGFVDLNSLRQRHDSFRSSVGTYSMNSSRQTRDTEKDEFW	486
mouse	eEF-2K	449	-DLDDPEPREHG--HSNGNR-RHEDEDSLGS-SCRVCVETWNLLNPSRL	493
human	eEF-2K	495A.....EK.....I.....	532
C.elegans	eEF-2K	487	KVLRKQSVPANILSLQLQQAANLENDEDVPQVTGHQFVSLGQTHIDLSR	536
mouse	eEF-2K	494	HLPRPSAVALQVQRNALDLGRKIGK-----SVLGKVLAMVR	531

Figure 2B

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human	eEF-2K	533G.....Q.....V.....N.....	565
C.elegans	eEF-2K	537	YHELGRFVEVDS EHKEMLEGS ENDARVPIKYD KQSAIFHL DIARKCGILE	586
mouse	eEF-2K	532	YHEGGRFCEKDEE-----WDR E SAIFHLEHAADLGELE	564
human	eEF-2K	566	596
C.elegans	eEF-2K	587	AVLTSAHIVLGLPHEL LKE TVDD LFPNGFGEQ ENGIRADKGQKPCDLEE	636
mouse	eEF-2K	565	AIVGLGLMYSQ LPHH ILADVSLKE-----TEENKTK-----	595
human	eEF-2K	597Q.....S.Q.....L.....	645
C.elegans	eEF-2K	637	FGSDILMEIAAEMGDKGAMLYMAHAYETGQH LGNRR TDYKKSIDWYQ RVV	686
mouse	eEF-2K	596	-GFDYLLKAAEAGDRHSMILVARAFDTGLNLSPDRCDWSEALHWYNTAL	644
human	eEF-2K	646	-----M.....M.....R.MM.....F.....Y..E.D.....	689
C.elegans	eEF-2K	687	GFQEEELSDCCGKTTFS SFAP LTRHEILAKMAEMYKEGGYGLNQD FERA	736
mouse	eEF-2K	645	-----ETTDCEG-GEYDGIQDEPQYALLAREAEMLLTGGFGLDKNPQRS	688
human	eEF-2K	690Q.....	725
C.elegans	eEF-2K	737	YGLFNEAAEAAMEAMNGKLAN KYYE KAEMC-----GE	768
mouse	eEF-2K	689	GDLTYTQAAEAAMEAMKGRLANQYYEKAEEAWAQMEE	724

Figure 2C

601-1-098CIP

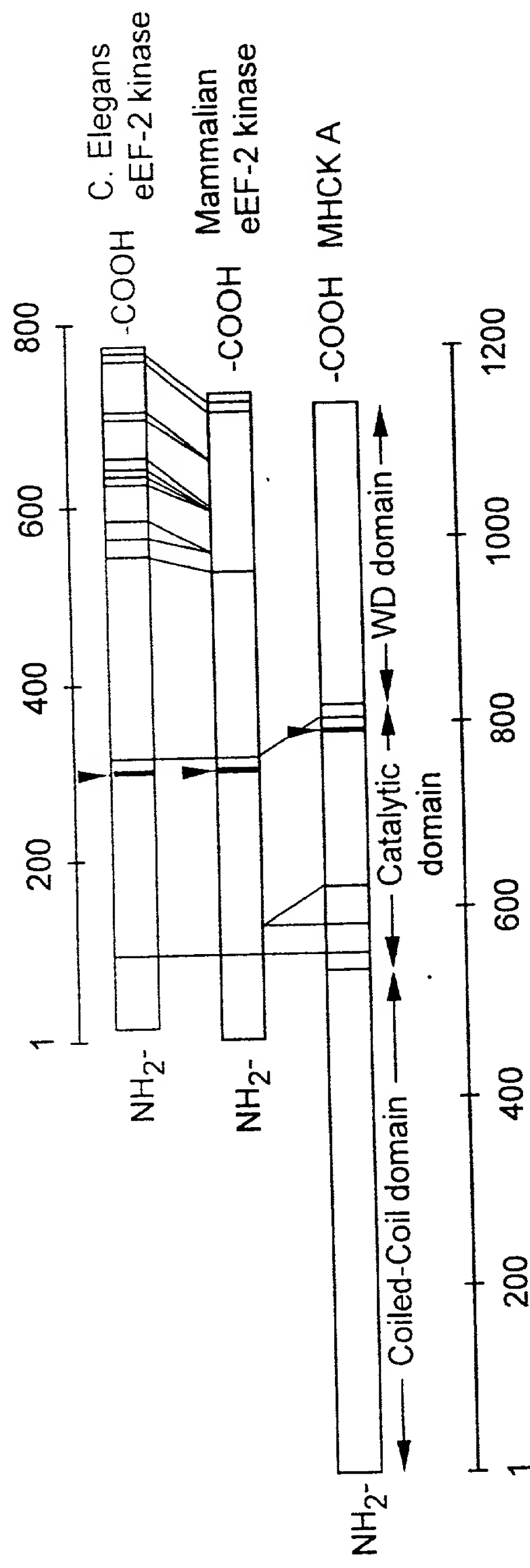


Figure 3

Current Biology

Figure 4

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121 gtccttggtt ggtggcccggt gccaccgctt cgggagacgc tttccgatag gtggctgcag
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Figure 5A

2941 tgaggtcttc atgtctgaag ctgggaaaat cagccagaag attaaagtat ggtttagtga
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Figure 5B

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Figure 5C

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LFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYHFIMAYHEKPVLPPLIILSHIVS
LFCCVCKRRKKDKTSDGPKLFLTEEDQKKLHDFEEQCVEMYFDEKDDKFNSGSEERIRVT
FERVEQMSIQIKEVGDRVNYIKRSLQSLDSQIGHLQDLSALTVDTLKTLTAQKASEASKV
HNEITRELSISKHLAQNLIDDVPVRPLWKKPSAVNTLSSSLPQGDRESNNPFLCNIIFMKD

Figure 6A

EKDPQYNLFGQDLPVIPQRKEFNIPEAGSSCGALFPSAVSPPELRQRRHGVEMLKIFNKN
QKLGSSPNSSPHMSSPPTKFSVSTPSQPSCKSHLESTTKDQEPIFYKAAEGDNIEFGAFV
GHRDSMDLQRFKETS NKIRELLSNDTPENTLKHVGAAGYSECCKTSTSLHSVQAESCSRR
ASTEDSPEVDSKAALLPDWLRDRPSNREMPSEGGTLNGLASPFPVLD TNYYYSAVERN
LMRLSQSIPFVPVPPRGEPTVYRLEESSPSILNNSMSSWSQLGLCAKIEFLSKEEMGGG
LRAVKVLCTWSEHDILKSGHLYIIKSFLPEVINTWSSIYKEDTVLHLCLREIQQQRAAQ
KLTFAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEFRKYNNNNGDEIIP
TLEEIMLAFSHWTYETRGELLVLDLQGVGENLTDPSVIKAEKRS CDMVFGPANLGEDA
IKNFRAKHHCNSSCCRKLKLPDLKRNDYTPDKIIFPQDESSDLNLQSGNSTKESEATNSVR
LML

Figure 6B

cgggcgcgggcgcgcgtccctgtggccagtcaccggaggaggtgggtgcacaattatgaaggactcggcttctgctgtagcggccggagctgagttagttctgagaagggttc
cctgggcgttcttctgtccggcgccctctgtctgcgcctccggagacgcttcccgatagatggctacaggccgcggaggaggaggagggttgagttgctgccccttccggagtc
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cgaatcaagcagttgcttggaaaagggtctattaaaagctgcagttacaactggagcctggattttaactggaggagtaaacacagggtgtggcaaacatgttggagatgccttc
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ttaaatctttaaagaaatgaaataaaatttattgtttacagataaaaaaa

Figure 7A

MSQKSWIESTLTKRECVYIIPSSKDPHRCLPGCQICQQLVRCFCGRLVKQHACFTA
SLAMKYSDVKLGDHFNQAIEEWSVEKHTEQSPTDAYGVINFQGGSHSYRAKYVRL
SYDTKPEVILQLLLKEWQMELPKLVISVHGGMQKFELHPRIKQLLGKGLIKA AVT
TGAWILTGGVNTGVAKHVGDALKEHASRSSRKICTIGIAPWGVNIENRNDLVGRDVV
APYQTLNPLSKLNVNLNLSHSHFILVDDGTVGKYGAEVRLRRELEKTINQQRIHAR
IGQGVPPVVALIFEGGPNVILTVLEYLQESPPVPVVVCEGTGRAADLLAYIHKQTEEG
GNLPDAAEPDIISTIKKTFNFGQNEALHLFQTLMECMKRKELITVFHIGSDEHQDID
VAILTALLKGTNASAFDQLILTLAWDRVDIAKNHVFVYGQQWL VGSLEQAML DAL
VMDRVAFVKLLIENGVS MHKFLTIPRLEELYNTKQGPTNPMLFHLVRDVKQGNLP
PGYKITLIDIGLVIEYLMGGTYRCTYTRKRFRLLIYNSLGGNNRRSGRNTSSSTPQLR
KSHESFGNRADKKEKMRHNHFIKTAQPYRPKIDTVMEEGKKKRTKDEIVDIDDPE
TKRFPYPLNELLIWACLMKRQVMARFLWQHGEESMAKALVACKIYRSMAYEAKQ
SDLVDDTSEELKQYSNDFGQLAVELLEQSFRQDETMMAMKLLTYELKNWSNSTCLK
LAVAAKHRDFIAHTCSQMLLTDMWWMGRRLMRKNPGLKVILSILVPPAILLLEYKT
KAEMSHIPQSQDAHQMTMDDSENNFQNITEEIPMEVFKEVRILDSNEGKNEMEIQM
KSKKLPITRKFYAFYHAPIVKFWFNTLAYLGFLMLYTFVVLVQMEQLPSVQEWIVI
AYIFTYAIEKVVREIFMSEAGKVNQKIKVWFSDYFNISDTIAISFFIGFGLRFGAKWNF
ANAYDNHVFVAGRLLIYCLNIIFWYVRLLDFLAVNQQAGPYVMMIGKMMVANMFYIV
VIMALVLLSFGVPRKAILYPHEAPSWTLAKDIVFHPYWMIFGEVYAYEIDVCANDS
VIPQICGPGTWLTPFLQAVYLFVQYIIMVNLLIAFFNNVYLQVKAISNIVWKYQRYH
FIMAYHEKPVLPPLIILSHIVSLFCCICKRRKKDKTSDGPKLFLTEEDQKKLHDFEE
QCVEMYFNEKDDKFHSGSEERIRVTFERVEQMCIQIKEVGDRVNYIKRSLQSLDSQI
GHLQDLSALTVDTLKTLTAQKASEASKVHNEITRELSISKHLAQNLIDDGPVRPSV
WKKHGVVNTLSSSLPQGDLESNNPFHCNILMKDDKDPQCNIFGQDLPAVPQRKEF
NFPEAGSSSGALFPSAVSPPELRQRLHGVVELLKIFNKNQKLGSSSTSIPHLSSPPTKFF
VSTPSQPSCKSHLETGTDQETVCSKATEGDNTEFGAFVGHRDSMDLQRFKETS
KIKILSNNNTSENTLKRVS LAGFTDCHRTSIPVHSKQEKISRRPSTEDTHEVDSKAA
LIPVWLQDRPSNREMPSEEGTLNGLTSPFKPAMDTNYYYSAVERNNLMRLSQSIPF
TPVPPRGEPVTVYRLEESSPNILNNSMSSWSQLGLCAKIEFLSKEEMGGGLRRRAVK
VQCTWSEHDILKSGHLYIISFLPEVVNTWSSIYKEDTVLHLCLREIQQQRAAQKLT
FAFNQMKPKSIPYSPRFLEVFLLYCHSAGQWFAVEECMTGEF
RKYNNNNGDEIPTNTLEEIMLAFSHWTYEYTRGELLVLDLQGVGENLTDPSVIKA
EEKRSCDMVFGPANLGEDA IKNFRAKHHCNSCCRKLKLPDLKRNDYTPDKIIFPQD
EPSDLNLQPGNSTKESESTNSVRLML

Figure 7B

ESAEPLTQSDKRETSHTTAAATGRSSHADARECAISTQAEQEAQTLQTSTDSVKEGNTNCKGEGMQVN
TLFETSQVPDWSDPPQVQVQETVRETISCSQMPAFSEPAAGEESPFTGTTISFNLGGVHKENASLAQHSEV
KPCTCGPQQEEKQDRDGNIPDNFREDLKYEQISEANDETMSPGVFSRHLPKDARADFREPVAVSVASPEP
TDTALTLENVCDEPRDREAVCAMECFEASDQGTCTDIDSLVGTPVDNYSPQEICSVDTELAEQONKVSD
LCSSNDKTLVFFQTQVSETSVSTCKSSKDGNSVMSPLFISTFTLNISHTASEGATGENLAKVEKSTYPLAS
TVHAGQEOPSPNSGGLEDQLLSENPNLVQFKEGGDKSPSPAADTTATPASYSSIVSFPWEKPTTLTAN
NECFQATRETVTIATEVHPAKYLAVSIPEDKHAGGTEERFPRASHEKVSQFPSQVVDHILSGATIKSTKEL
LCRAPSVPGVPHHVLQLPEGEGCSNPLQVDNLSGDKSQTVDRADFRSYEENFQERGSETKQGVQQQSL
SQQGSLAPDFQQSLPTTSAAQEERNLVPTAPSPASSREGAGQRSWGTRVSVVAETAAGEEDSQALSNVPS
LSDILLESKEYRPGNWEAGNKLKIITLEASASEIWPPRQLTNSEKASDGLIIPDKVWAVPDSLKADAVV
PELAPSEIAALAHSPEDAESALADSRESHKGEEPTISVHWRSLSSRGFSQPRLLESSVDPVDEKELSVTDSLS
AASETGGKENVNVNSQDQEEKQLKMDHTAFFKKFLTCPKILESSVDPIDEISVIEYTRAGKPEPSETTPQGA
REGGQNSDGNMGHEAEIQSAILQVPCLOQTILSENRISSQEGSMKQEAEQIQPEEAKTAIWQVLQPSEGG
ERIPSGCSIGIQESSDGSLSGEAEQSKKDKAELISPTSSCLPIMTHSSLGVDTHNSTGQIHDVPENDIVEP
RKRQYVFPVSQKRGTIENERGKPLPSSPDLTRFPCTSSPEGNVTDFLISHKMEEPKEIQLQIGETKPPSSSSSS
AKTLAFISGERELEKAPKLLQDPCQKGTLCACKSREREKSLEARAGKSPGTLTAVTGSEEVKRPKEAPGS
GHLAEGVKKKILSRVAALRLKLEKENIRKNSAFLKKMPKLETSLSHTEEKQDPKPKPSCKREGRAPVLLK
KIQAEEMFPEHSGNVKLSQCQFAEIHEDSTICWTKDSKSIQVQRSAGDNSTVSFAIVQASPKDQGLYYCCIK
NSYGKVTAEFNLTAEVLKQLSSRQDTKGCEEIEFSQLIFKEDFLHDSYFGGRLRGQIATEELHFGEGVHRK
AFRSTVMHGLMPVFKPGHACVLKVHNAIAYGTRNNDELIQRNYKLAQECYVQNTARYYAKIYAAEAQ
PLEGFGEVPEIPIFLIHRPENNIPYATVEEELIGEFVKYSIRDGKEINFLRRESEAGQKCCTFQHWVYQKTS
CLLVTDMMQGVGMKLTVDVGIATLAKGYKGFKGNCSTFIDQFKALHQC�KYCKMLGLKSLQNNNQKQK
QPSIGKSKVQTNSTMTVKKAGPETPGEKKT

Figure 8B

1 atgtcccaga aatcttggat taaaggagta ttgacaaga gagaatgtag cacaatcata
 61 cccagctcaa aaaatcctca cagatgtact ccagtatgcc aagtcigcca gaatttaate
 121 aggtgttact gtggccgact gattggagac catgetggga tagattatte ctggaccate
 181 tcagetgcca agggtaaaga aagtgaacaa tggctgttg aaaagcacac aacgaaaage
 241 ccaacagata cttttggcac gattaatttc caagatggag agcacacca teatgccaag
 301 tatattagaa cttcttatga tacaaaactg gatcatctgt tacatttaac gttgaaagag
 361 tggaaaatgg aactgcccac gcttgtgatc tcagtccatg ggggcatcca gaactttact
 421 atgcecteta aatttaaaga gattttcage caaggttgg ttaaagctgc agagacaaca
 481 ggagcgtgga taataactga aggcatacat acagtgtcca agcatgttgg gcatgcectg
 541 aaatccatt cctctcattc ctgagaaaa atctggacag ttggaatccc tectggggt
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 661 gataaccccc tcagcaaget cacaacactc aacagcatgc actgcactt catectgtct
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 1501 gacattggat tagtagtaga atacctcatt ggtagagcat atgcagcaa ctacactaga
 1561 aaacatttca gageccteta caacaacctc tacagaaaat acaagcaca gagacactcc
 1621 tcaggaaata gaaatgagtc tgcagaaagt acgtgcact cccagttcat tagaactgca
 1681 cagecataca aattcaagga aaagtctata gtcttcata aatcaaggaa gaagcaaaa
 1741 gaacaaaatg tatcagatga cctgagttc actggtttc ttaccetta caatgacctg
 1801 ctggtttggg ctgtctgat gaaaaggcag aagatggcta tgttctctg gcagcatgga
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 1981 tttggccage ttgctctgga cttgttggag aaggcattca agcagaatga gcgatggcc
 2041 atgacgtgtg tgacgtatga actcaggaac tggagcaatt cgacctgcat taaactggcc
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 2221 attttaccac ccaccattt gacactgga tttaaaagca aagetgagat gtcacatgtt
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 2521 ttectcatgc ttttactta caccgtgtg gtggagatgc agccccagcc cagcgtgcag
 2581 gagtggcttg ttagcattta catcttcacc aatgtattg aggtggctag ggaggtgagt
 2641 atttcagaac ctgggaagt tacccaaaag gtgaaggat ggattagtga gtactggaac
 2701 ttaacagaaa ctgtggccat tggctgttt tcagctggt tegtctctg atggggtgac
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 2821 eggtctctg actctttgc tgtgaatcaa catgcaggtc catatgtgac catgattgca
 2881 aaaatgacag caaacatgt ctatattgtg atcatcatgg ccatagtcct gctgagctt
 2941 ggagtggcag gcaaggccat ctttgcga aaagagccac catcttggag tctagctega
 3001 gatattgtat ttgagccata ctggatgata tacggagaag tetatgctgg agaaatagat
 3061 gtttgtcaa gccagccate ctgcctctt ggttctttt ttactccatt ctgcaagct
 3121 gtctacctct tctgcaata tatcatcatg gtgaacctgt tgattgttt ctcaacaac
 3181 gtttacttag atatggaate catttcaat aacctgtgga aatacaaccg ctatcgtac

Figure 9A

3241 atcatgacct accacgagaa gceetggetg cccccacete teatcetget gagceacgtg
 3301 ggeettetec tccgeceet gtgetgtcat egagctete acgaccaaga agagggtgac
 3361 gttgattaa aactctacct cagtaaggag gatetgaaaa aacttcatga ttttgaggag
 3421 cagtgcgtgg aaaaatactt ccatgagaag atggaagatg tgaattgtag ttgtaggaa
 3481 cgaatcegag tgacatcaga aagggttaca gagatgtact tccagctgaa agaaatgaat
 3541 gaaaagggtgt cttttataaa ggactectta ctgtctttgg acagccaggt gggacacctg
 3601 caggatctet ctgeectgac tgtggatacc ctgaaagtec ttctgtctgt tgacactttg
 3661 caagaggatg aggetctect ggccaagaga aagcattcta ctgcaaaaa acttccccac
 3721 agctggagca atgtcatctg tgcagagggt ctaggcagca tggagatcgc tggagagaag
 3781 aaataccagt attatagcat gcectctctt ttgetgagga gceetggetg aggcgggcat
 3841 cccccaagag tgcagagggg ggcacttctt gagattacaa acagtaaaag agaggetaca
 3901 aatgtaagaa atgaccagga aaggcaagaa acacaaagta gtatagtgtt ttctggggtg
 3961 tctectaaca ggcaagcaca ctcaaagtat ggccagtttc ttctggctcc ctetaatcta
 4021 aagegagtte cttttcage agaaactgtc ttgectctgt ccagaccete tgtgccagat
 4081 gtgtggcaa ctgaacagga catccagact gaggttctt ttcatctgac tgggcagacc
 4141 ccagtgtct ctgactgggc atcagtggtt gaaccaagg aaaagcaaga gctattgtct
 4201 cacttactgg atggacaaga caaggcagag caagtgtac ccacttgag ttgcacacct
 4261 gaacctatga caatgagete cctctttcc caagcaaga tcatgcaaac tggaggtgga
 4321 tatgtaaaact gggcatttcc agaagggtat gaaactgggt tgtttagcat caagaaaaag
 4381 tggcaaacct gcttgcete cacttgtac agtgattct ctggagtgac acagcaccag
 4441 aagcagggcc aggcagete cctatctgat aactcaacaa gatcgccca gagtagtgaa
 4501 tgetcagagg tgggaccatg gcttcagcca aacacatct tttggatcaa tctctcgc
 4561 agatacagge cctcgetag gactcatagt tttagattcc ataaggagga gaaattgatg
 4621 aagatctgta agattaaaaa tcttcaggc tcttcagaaa tagggcaggg agcatgggtc
 4681 aaagcagaaa tgctaacca agacaggaga ctgtcaaga aaaagaagaa tactcaagga
 4741 ctccaggtgc caatcataac agtcaatgcc tgetctcaga gtgaccagt gaatccagag
 4801 ccaggagaaa acagcatete tgaagaggag tacagcaaga actggttcc agtgtccaa
 4861 tttagtcaca caggtgtaga accttataca catcagaaaa tgaactaa agaaattgga
 4921 caatgtgta tacaatcag tgattaccta aagcagctc aagaggatct cagcaaaaac
 4981 tctttgtgga attccaggag caccaacete aataggaact cctgtctgaa aagttcaatt
 5041 ggagttgaca agatctcagc ctcttataaa agectcaag agectacca tcatattca
 5101 gccattgaaa ggaataattt aatgaggett tctcagacca taccatttac accagtccaa
 5161 ctgtttgcag gagaagaaat aactgtctac aggttggagg agagtccccc tttaacctt
 5221 gataaaagca tgctctctg gtctcagctt gggagagcgg caatgatcca ggtattgtcc
 5281 cgagaggaga tggatggggg cctccgtaaa gctatgagag tctcagcac ttggtctgag
 5341 gatgacatc tcaagccggg acaagtttc attgtcaagt ccttcttcc tgaggttgtg
 5401 cggacatgge ataaaatctt ccaggagage actgtgcttc atctttgect cagggaaatt
 5461 caacaacaaa gagctgetca aaaattgatc tataccttca accaagtga accacaaacc
 5521 atacctaca caccaaggtt cctggaagtt ttcttaatct actgcatc agccaaccag
 5581 tgggtgacca ttgagaagta tatgacaggg gagttccgga agtataacaa caacaatggt
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 5701 tatgagtaca ctgggggaga gctgtggtt ttagatttgc aaggtgttgg agaaaatttg
 5761 acagatccat ctgttataaa acctgaagtc aaacaatcaa gaggaatggt gtttgaccg
 5821 gccatttgg gggaagatgc aattagaaac ttcattgcaa aacatcattg taactctgc
 5881 tgccggaagc tcaaacctcc gatttataaa agaaatgact attccctga aaggataaat
 5941 tccaccttg gacttgagat aaaaatagaa tcagctgagg agctccagc aaggagagc
 6001 ggtagaaatt cccagaaga tgatgtgcaa ctataaaaag ggaggagcaa gaagatccca
 6061 gtgttgcct tgcctgccag gaaetctgt ataacataga ttgatcaac tgatgttgat
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 6301 tgtgtacete attgctttag ctggtcactt ggaacttgg agcagaatcc tgcacattaa
 6361 aggatgggtt tgggggggat acatttattt tttttctca ctatgtatgc agactggacc
 6421 cctactact attgtcacc tcaaccacag attgtattta tgtetatata tatgtcata

Figure 9A

6481 aaaagtatg tgatttecte ctctgtcttt tcacaacat aggactttga atagcaatga
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 6601 taccaagtat actggtgaaa tctcgatggg ttccagatat tgcagtga tcataatgatg
 6661 cctggatatt tcaggtttct gtaaaagaaa gggaaacctt aaacaaatac ccttccatat
 6721 ataatatata tggaataatg atattatata ttttttata tatataatat atatggaata
 6781 tatatattat atatataaaa tacatatgga atatatatat tttatatata tatatatatt
 6841 tttatttttg agatggagtt tcactctttt taccagget ggagtgeaat gatgcatct
 6901 cactgeaace tctgcctccc gggttgagc gattcttggt tctcagttt cgggtagct
 6961 gggactacag gtgtgcacca ctatgctgg ctaattttgt atttttagta gagatgggg
 7021 ttcacatgt tggcagget ggtcctaaac tctgacctc agatgatcca cctgcttgg
 7081 cttcccaaag tgcgggatt acaggcgtga gccactgcgc ctggcctttt tttttttt
 7141 tttaaacgag aacaagaata tgaagaactg gaaatcatta agaaagggtt tcccttctt
 7201 aaagctcagg ggtaactatta gttaggagtt gactaacctc accgttaaaa caccactct
 7261 ccttccaaag ttgtatatat aatattgcag gttaaattac tttatgtcag gtcctatgaa
 7321 gaaagatacg gtttcagact gaaaacatgt ttcacaggtg tttgttctt tccagagcag
 7381 agttccctat tccctggca taaagaatgt atatataatt tgaaatatgg ctgagaacat
 7441 gtcattggtt tgtgagget aaggtgaage actctggca gccacactgt gtagtgtatt
 7501 tgagggatca gtcacctc ttgtatgtg ggctgggtt cctacctcg aacaagcacc
 7561 agctttcac acaaggagag atgtggggtt gggagctc tccctctct attgcatct
 7621 cttcttatt ataagctgtt ccagttcaca ggcagcaaac ctctgggtt tgaaaaattc
 7681 caactattt ttatcttaa tctgacatt agctgactg ctagtactt tcttttaaa
 7741 atctacactc ttgcattctt aggcatacag gggaaatgtt gaaaaggaag gtggaaaacc
 7801 aagaatttag ttgccaatg attgctctg attcttgtaa gtttgagtt cacaagggt
 7861 aatttatcc cttttactt gggtttggg gtggtggaaa ggggaaatt tgggtgattt
 7921 gttgattgga aatgaggata aaatgttaat actttttgg ggacttaaca actttactt
 7981 attctacaag tcagtaaagg aacaattgtt actacctca gtgctgact caactatgga
 8041 aagaggcaga gtttcttgc ccaattgcca aactaaagac atcagttcat tggtaata
 8101 tttgtacct ggaatggaac ttgaaagcaa atacatttg atttcaaatt tcaaaaaa

Figure 9A

MSQKSWIKGVFDKRECSTIIPSSKNPHRCTPVCQVCQNLIRCYCGRLIGDHAGIDYS
WTISAAKGKESEQWSVEKHTTKSPTDTFGTINFQDGEHTHHAKYIRTSYDTKLDHL
LHLMLKEWKMEPKLVISVHGGIQNFTMPSKFKEIFSQGLVKAAETTGAWIITEGI
NTVSKHVGDAKSHSSHSLRKIWTVGIPPWGVNIENQRDLIGKDVVCLYQTLDNPLS
KLTTLNSMHSFILSDDGTVGKYGNEMKLRRNLEKYLSQLKIHCRRSRQGVVVG
VVEGGPNVILSVWETVKDKDPVVVCEGTGRAADLLAFTHKHLADEGMLRPQVKE
EIIICMIQNTFNFSKQSKHLFQILMECMVHRDCITIFDADSEEQQDLDLAILTALLK
GTNLSASEQLNLAMAWDRVDIAKKHILIYEQHWKPDALQAMSDALVMDRVDFV
KLLIEYGVNLHRFLTIPRLEELYNTKQGPTNTLLHHLVQDVKQHTLLSGYRITLIDI
GLVVEYLIGRAYRSNYTRKHFRALYNNLYRKYKHQRHSSGNRNESAESTLHSQFIR
TAQPYKFKEKSIVLHKSRRKKSKEQNVSDDPESTGFLYPYNDLLVWAVLMKRQKMA
MFFWQHGEETATVKAVIACILYRAMAHEAKESHMVDDASEELKNYSKQFGQLALD
LLEKAFKQNERMAMTLLTYELRNWSNSTCLKLAVSGGLRPFVSHCTCTQMLLTDM
WMGRLKMRKNSWLKIIISIILPPTILTLEFKSKAEMSHVPQSQDFQFMWYYSDQNA
SSSKESASVKEYDLERGHDEKLDENQHFGLSEGHQHLPWTRKVYEFYSAPIVKFW
FYTMAYLAFLMLFTYTVLVEMQPQPSVQEWLVSIYIFTNAIEVVREVSISEPGKFTQ
KVKVWISEYWNLTETVAIGLFSAGFVLRWGDPPFHTAGRLIYCIDIIFWFSRLLDFF
AVNQHAGPYVTMIAKMTANMFYIVIIAIVLLSFGVARKAILSPKEPPSWSLARDIV
FEPYWMIYGEVYAGEIDVCSSQPSCPPGSFLTFLQAVYLFVQYIIMVNLLIAFFNNV
YLDMESISNNLWKYNRYRYIMTYHEKPWLPPPLILLSHVGLLLRRLCCHRAPHDQ
EEGDVGLKLYLSKEDLKKLHDFEEQCVEKYFHEKMEDVNCSCERIRVTSEVTE
MYFQLKEMNEKVSFIKDSLLSLDSQVGHLLQDLSALTVDTLKVLSAVDTLQEDDEALL
AKRKHSTCKKLPHSWSNVICAEVLGSMEIAGEKKYQYYSMPSSLLRSLAGGRHPP
RVQRGALLEITNSKREATNVRNDQERQETQSSIVVSGVSPNRQAHSKYGQFLLVPS
NLKRVPFSAETVLPLSRPSVPDVLATEQDIQTEVLVHLTGQTPVVSVDWASVDEPKE
KHEPIAHLLDGQDKAEQVLPTLSCTPEPMTMSSPLSQAKIMQTGGGYVNWAFSEG
DETGVFSIKKKWQTCLPSTCDSRSSRSEQHQKQAQDSSLSDNSTRSAQSSECSEVGP
WLQPNTSFWINPLRRYRPFARSHSFRFHKEEKLMMKICKIKNLSGSSEIGQGAWVKA
KMLTKDRRLSKKKKNTQGLQVPIITVNACSQSDQLNPEPGENSISEEEYSKNWFTV
SKFSHTGVEPYIHQKMKTKKEIGQCAIQISDYLKQSQEDLSKNSLWNSRSTNLNRNSL
LKSSIGVDKISASLKSPQEPHHHYSIAIERNNLMRLSQTIPFTPVQLFAGEEITVYRLE
ESSPLNLDKSMSSWSQRGRAAMIQVLSREEMDGLRKAMRVVSTWSEDDILKPGQ
VFIVKSFLPEVVRTWHKIFQESTVLHLCLREIQQQRAAQKLIYTFNQVKPQTIPYTP
RFLEVFLIYCHSANQWLTIEKYMTGEFRKYNNNNGDEITPTNTLEELMLAFSHWTY
EYTRGELLVLDLQGVGENLTDPSVIKPEVKQSRGMVFGPANLGEDAIRNFIKHHHC
NSCCRKLKLPDLKRNDYSPERINSTFGLEIKIESAEPPARETGRNSPEDDMQL

Figure 9B

[illegible]

Figure 10A

[illegible]

Figure 10A

T02121 2523860

601-1-098CIP

MEVAWL VYVLGQQPLARQGEQSR LVPGRGLV LWPGLPRSSWP AVDLAPARPRGPLICHTGHEQAGREPG
PGSSTKGPVLHDQDTRCAFLPRPPGLQTRRYCRHQGRQCSGLGAGPGAGTWAPAPPGVSKPRCPRARPGEGQQQ
VTTARPPAINRGARQPRAGAAAAGRGPGAGAWRTGEAAASAGPAVGEAGMGSRRAPTRGWGAGGRSGAGGDGE
DDGPVWIPSPASRSYLLSVRPETSLSSNRLSHPSSGRSTFCSHIAQLTEETQPLFETTLKSRSVSESDVRFTCIVTGYPEP
EVTWYKDDTELDRYCGLPKYEITHQGNRHTLQLYRCREEDAAIYQASQNSKGIVSCSVLEVGMTTEYKIHQRWF
AKLKRKAAAKLREIEQSWKHEKAVPGEVDTLRKLSPDFRQRRRLSGAQAPGPSVPTREPEGGTLAAWQEGETETA
QHSGGLINSFASGEVTTNGEAAPENGEDGEHGLLTICDAMELG PQRALKEESGAKKKKKDEESKQGLRKPELEKA
AQRRSEN CIPSSDEPDSCGTQGPVGEVQVQTQPRGRAARGPGSSGTDSTRKPASAVGTPDKAQKAPGPGQEYVF
SLKDMYLENTQAVRPLGEEGPQTL SVRAPGESPKGKAPLRARSEGVP GAGPQPTHSLTPQPTRPFNRKRFA PPKPKG
EATTD SKPISSLSQAPECGAQS LGKAPPQASVQVPTPPARRRHGTRDSTLQGA GHRTPEGVLECCQTTTAPTMSASSSS
DVASIGVSTSGSQGHIEPMDMETQEDGRTSANQRTGSKKNVQADGKIQVDGTRGDGTQTAQRTRADRKTQVDAGT
QESKR PQSDRSAQKGM MTQGRAETQLETTAQEGEKIQEDRKAQADKGTQEDRRMQEGKMGQEKGTQSEGSAPTA
MEGQSEQEVATSLGPPSRTPKLPTAGPRAPLNIECFVQTPEGSCFPKPGCLPRSEEA VVTASRNHEQTVLGPLSGNL
MLPAQPPHEGSVEQVGGERCRCRGPQSSGPVEAKQEDSPFQCPKEERP GGVP CMDQGGCPLAGLSQEVPTMPSLP GTG
LTASPKAGPCSTPTSQHGSTATFLPSEDQVLMSSAPTLHLGLGTPTQSHPPETMATSSSEGACAQVPDVEGRTPGPRSC
DPGLIDSLKNYLLLLKLSTETSGAGGESQVGAATGGLVPSATLTPTVEVAGLSPTSRRILERVENNNHLVQSAQTLL
LSPCTSRRLTGLLDREVQAGRQALAAARGSWGPGPSSLTVPAIVVDEEDPGLASEGASEGEVSLGPGLLGASQES
SMAGRLGEAGGAAPGQGPSAESIAQEPSQEEKFPGEALTGLPAATPEELALGARRKRFLPKVRAAGDGEATTPEER
ESPTVSPRGRKSLVPGSPGTPGRERRSPTQGRKASMLEVPRAEEELAAGDLGSPKAGGLDTEVALDEGKQETLAKP
RKAKDLLKAPQVIRKIRVEQFPDASGSLKLWCQFFNILSDSVLTWAKDQRPVGEVGRSAGDEGPAALAIVQASPVDC
GVYRCTIHNEHGSASTDFCLSP E VLSGFISREEGEVGEIEMTPMVFAKGLADSGCWGDKLFGRLVSEELRG GYG C
GLRKASQAKVIYGLEPIFESGRTCHIKVSSLLVFGPSSETSLVGRNYDVTIQGCKIQNMSREYCKIFAAEARAAPGFGEV
PEIPLYLIYRPANNIPYATLEEDLGKPLEYCSREWGCAEAPTASGSSEAMQKCCQTFQHWLYQWTNGSFLVTDLAGV
DWKMTDVQIATKLRGYQGLKESCFPALLDRFASHQCNA YCELLGLTPLKGPEAAHPQAKAKGSKSPSAGRKGSQ L
SPQPQKKGLPS PQGTRKSAPSSKATPQASEPVTTLQLGQPPTQEEGSKAQGM R

Figure 10B

Figure 11A

MNNQKVVAVLLQECKQVLDQLLLEAPDVSEEDKSEDQRCRALLPSELRTLIQEAKEMKWPFVPEK
WQYKQAVGPEDKTNLKDVGAGLQQLLASLRASILARDCAAAAIVFLVDRFLYGLDVSGKLLQVA
KGLHKLQPATPIAPQVVIRQARISVNSGKLLKAEYILSSLISNNGATGTWLYRNESDKVLVQSVCIQI
RGQILQKLGMWYEAAELIWAIVGYLALPQPDKKGLSTSLGILADIFVSMKNDYEKFKNNPQINLS
LLKEFDHLLLSAAEACKLAAAFSAYTPLFVLTAVNIRGTCLLSYSSNDCPPPELKNLHLCEAKEAFEI
GLLTRDDEPVTGKQKQELHSFVKAAFGLTTVHRRHLHGETGTVHAASQLCKEAMGKLYNFSTSSRSQ
DREALSQEVMSVIAQVKEHLQVQSFSNVDDRSYVPESFECRLDKLILHGQGFQKILDYTSQHHTSV
CEVFESDCGNNKNEQKDAKTGVCITALKTEIKNIDTVSTTQEKPHCQRDTGISSLMGKNVQRELRR
GGRRNWTHSDAFRVSLDQDVEETEPEPSDYSNGEAVFNKSLSGSQTSAAWSNLSGFSSASWEEVNY
HVDDRSARKEPGKEHLVDTQCSTALSEELENDREGRAMHSLHSQLHDLSLQEPNNDNLEPSQNQPQ
QQMPLTPFSPHNTPGIFLAPGAGLLEGAPEGIQEVNMGPRNTSAHRPSYRSASWSSDSGRPKNMG
THPSVQKEEAFEIIVEFPETNCDVKDRQKEQGEIEISERGAQTFFKASPSWVDPEGETAESTEDAPLD
FHRV LHNSLGNISMLPCSSFTPNWPVQNPDSRKSGGPVAEQGIDPDASTVDEEGQLLDSMDVPCTNG
HGSHRLCILRQPPGQRAETPNSSVSGNILFPVLSEDCCTTTEEGNQPGNMLNCSQNSSSSVWWLKSP
AFSSGSSEGDSPWSYLNSSGSSWVSLPGKMRKEILEARTLQPDDEFKLLAGVRHDWLFQRLENTGV
FKPSQLHRAHSALLKYSKKSELWTAQETIVYLG DYLT VKKKGRQRN AFWVHHLHQEEILGRYVG
KDYKEQKGLWHHFTDVERQMTAQHYVTEFNKRLYEQNIPTQIFYIPSTILLILEDKTIKG CISEPYI
LGEFVKLSNNTKVVKTEYKATEYGLAYGHFSYEFSNHRDVVVDLQGWVTGNGKGLIYLTDPQIHVS
DQKVFTTNFGKRGIFYFFNNQHVECN EICHRLSLTRPSMEKP

Figure 11B

A	HeEF-2_kinase>	1	MLDD--EVLAKKASQPFGRG---	AMRECHPTKKSNFLHAQQWKASN--YVAMRELEPPVDR---	DVAFED---
	MHCK_B>	1	ACT--ATLAKQEPVPFAEG---	FRKATILD'S-----KSGASGRVVSIGKKPTPR---	PSVFEF---
	Melanoma_kinase>	1	SQLGLCAKEFLSKSEEMGG---	GRFAVRVOCTWS---EHDILKSEHIMTSSLEPEVNTWSSINKE	DTVLHCLRE
	Kidney_kinase>	1	QORGRAAMQQLSREEMDG---	GRKAMGVVSTWS---EDDLKPSQVETASSLEPEVVRTWHKIE	QESTVLHCLRE
	Muscle_kinase>	1	GDGK---TFGRVSEELRGGGYGC---	GRKASQAKVYSG---LEPFESGRICNVSSILLVFGPSSETSLVGRNYD	VTIQG
	Heart_kinase>	1	GGGR---IRGQAAEELHFG--EGVHRKATSTVHHG---	LMPFKPCHACVIVHNAIAYGTRNDELIOQRYKFAAQE	
	Lymphocyte_kinase>	1	MAQETINVYCDYLTVKKKG---	RQMAVWHHSH-----QBEILGRVYCDQKEQKGL---	WHHFTD---
	consensus	1	wt v i m s e G amRkafr l i g yvik y v y ed i		
			I		
			II		
	HeEF-2_kinase>	62	VRPOMEARLAGEENNRHKPPKQ--VIMQVCTHEIKDRP-GKPLSH--	HEHMECKVIKYNNSG---	FVRDIN-IR
	MHCK_B>	56	VKAQMIAGKADKNSFPKPKK--IEFLQSCVKEFDRT-SSDLICG-AEPM	IEGQIRKYNNSG---	FVSNL---ER
	Melanoma_kinase>	74	QQQRAAQLTFAEQMKPKSI--PYSREFEVLVYCH-SAGQFA--	RECOVTEHFRKYNNGD---	EILPTNG-LE
	Kidney_kinase>	74	QQQRAAQLTFTNOVKQOTI--PYTPREFEVLVYCH-SANQALT--	REKVTGEHFRKYNNGD---	EITPTNI-LE
	Muscle_kinase>	75	CKQNMSETECKIFAAEARAAPGFGNPEPPLVYRPANNIPAT--	SEDIQKPLESYCSREWGCAEAPTASGSSEAM	
	Heart_kinase>	73	CYQNTALVAKIAAEAOPLGFGNPEPPLVYRPENNIPAT--	SEETIGBHVKYSIRDG---	KEINFRRKSEAG
	Lymphocyte_kinase>	58	MEROMTACQVTEENKRLYEQNIPTQFYFPTSTILILEDKTIKGCIS	EPVILGEFVLSNNTK-----	VAKTYKAT
	consensus	81	v lQ akkw fn kp dip ml iflv r f lE yi gef kynnn g v dt		
			III		
			IV		
	HeEF-2_kinase>	130	LTPQAFSHTEERGHQLVIDVQGG--VG-----	LYTDPQIHET-----	GLALFFYSH-AGNRIC
	MHCK_B>	124	NTPQFSHTYVEHSHQLLVDLQGG--VG-----	PHYTDPQIHET-----	GVCFGICNLGQK-CFERFLDTH-KCNATC
	Melanoma_kinase>	145	EIMLAFSHWTVETRGELLVDLQGG--VG-----	ENLTDPSVIKAGEKRSQCDWVFGP--	NLGED-ATKNFRAKH-HCNSSC
	Kidney_kinase>	145	ELMLAFSHWTVETRGELLVDLQGG--VG-----	ENLTDPSVIKPEVKQSRGVFGP--	NLGED-ATKNFIAKH-HCNSSC
	Muscle_kinase>	154	QKQITFQHWLVYVINGSEFVTDIAG--VD-----	WKTVDVQIAIKLR-----	CYQGLKESCFPA-LIDRFASSH-QCNAYC
	Heart_kinase>	150	QKCCITFQHWVVKISSCLLVTDVQGG--VG-----	MKLTVDVGIAJLAK-----	CYKGFKNCSMT-FIDQFKALH-QCNKYC
	Lymphocyte_kinase>	132	EYGLATGHEFEVFSNHRDVIDLQGGWVTENGKGLIYLTDPQIHSEV	-----QKVFTINFGKRGIFYFENNQIVEGNEIC	
	consensus	161	afshwtyeyt g llvvdIqg vg d lTdpqi t d g fg gnlg gm f H CN C		
			V		
			VI		
	HeEF-2_kinase>	196	ESYGLAPF		
	MHCK_B>	190	QYINLQSH		
	Melanoma_kinase>	216	RKLKLPDR		
	Kidney_kinase>	216	RKLKLPDF		
	Muscle_kinase>	221	ELLGLTPS		
	Heart_kinase>	217	RMLGKSGF		
	Lymphocyte_kinase>	206	RLSLTRP		
	consensus	241	r l l l i		
			VII		
			VIII		

Figure 12

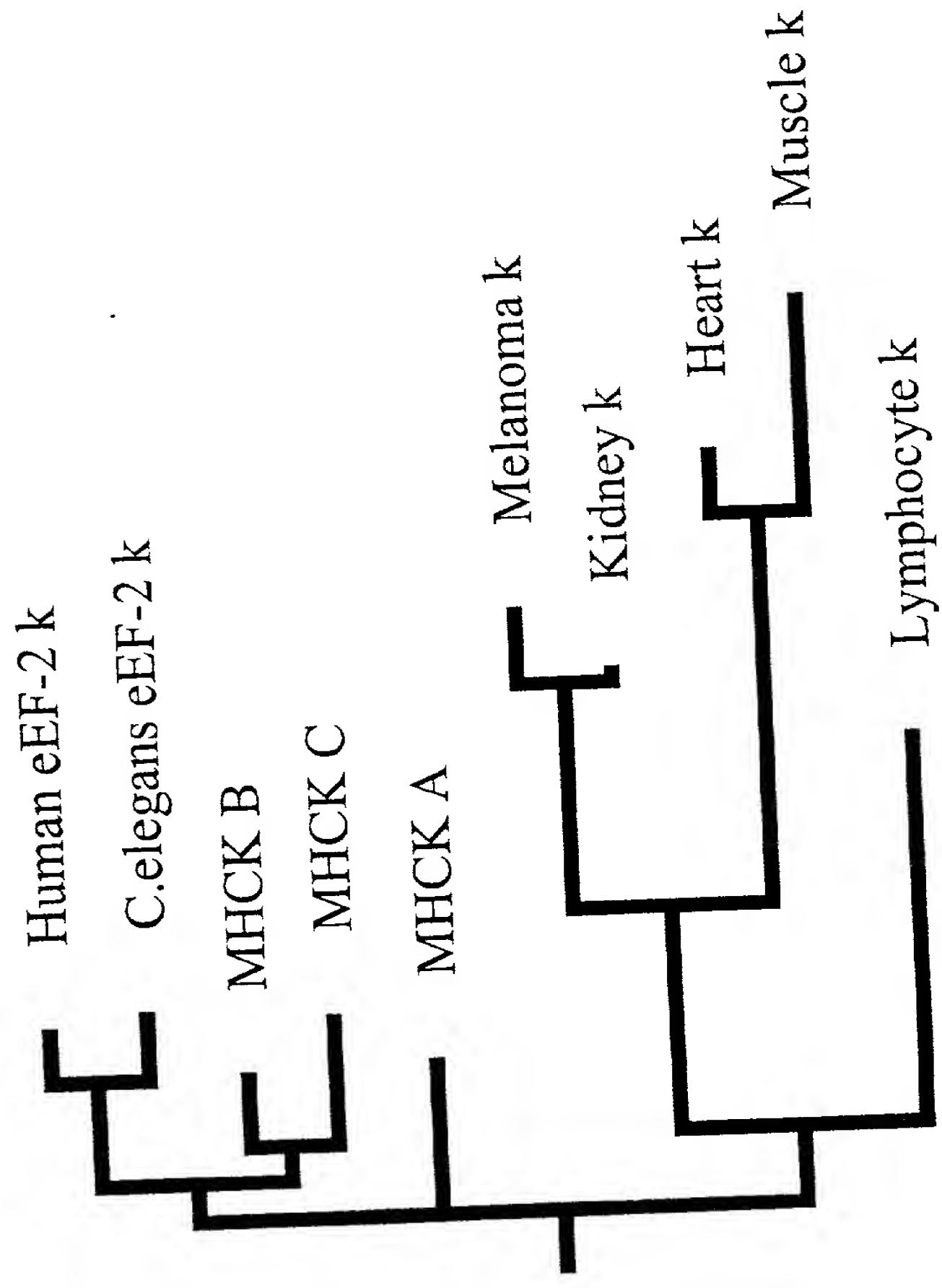


Fig. 1

Figure 13

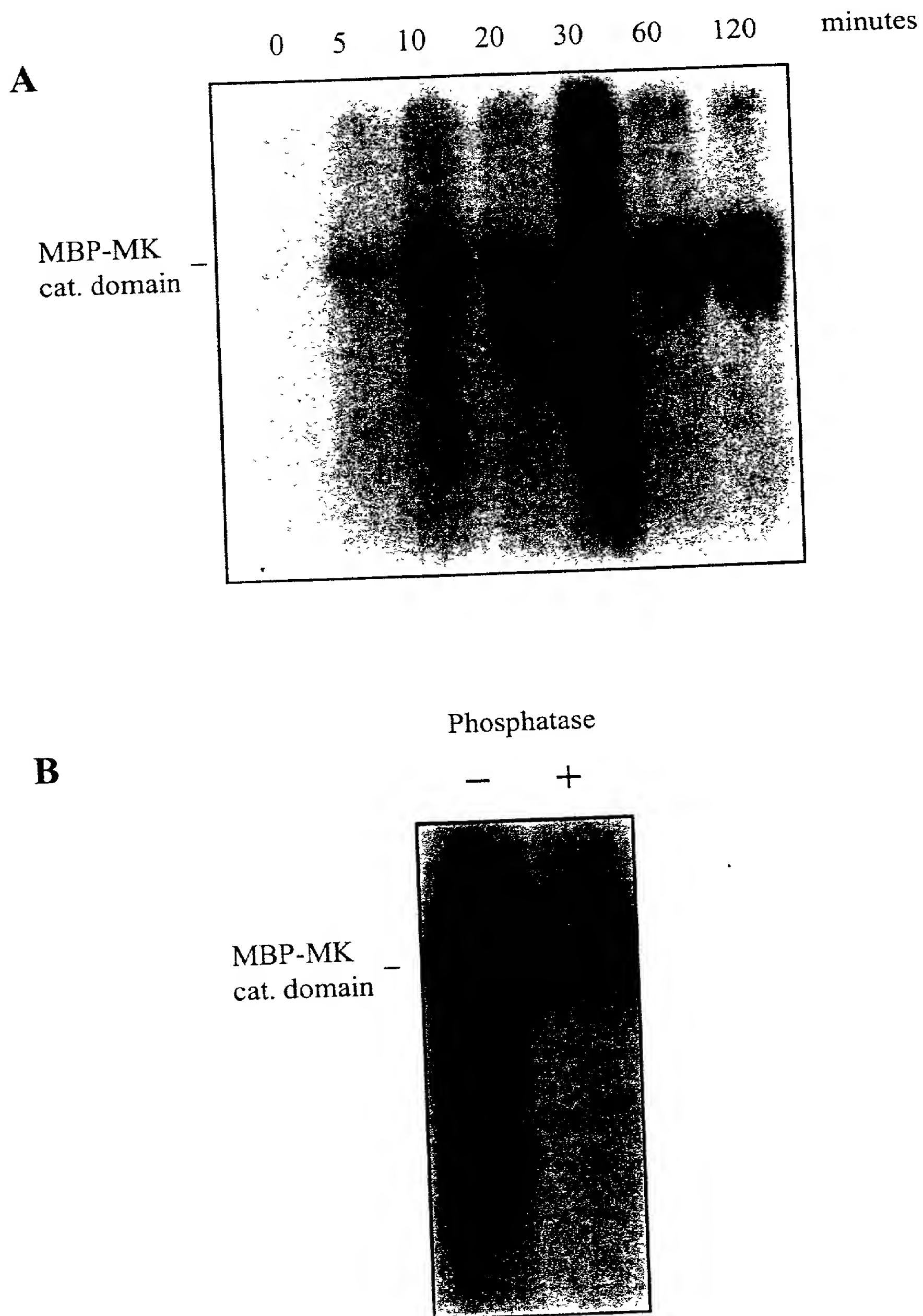


Figure 14

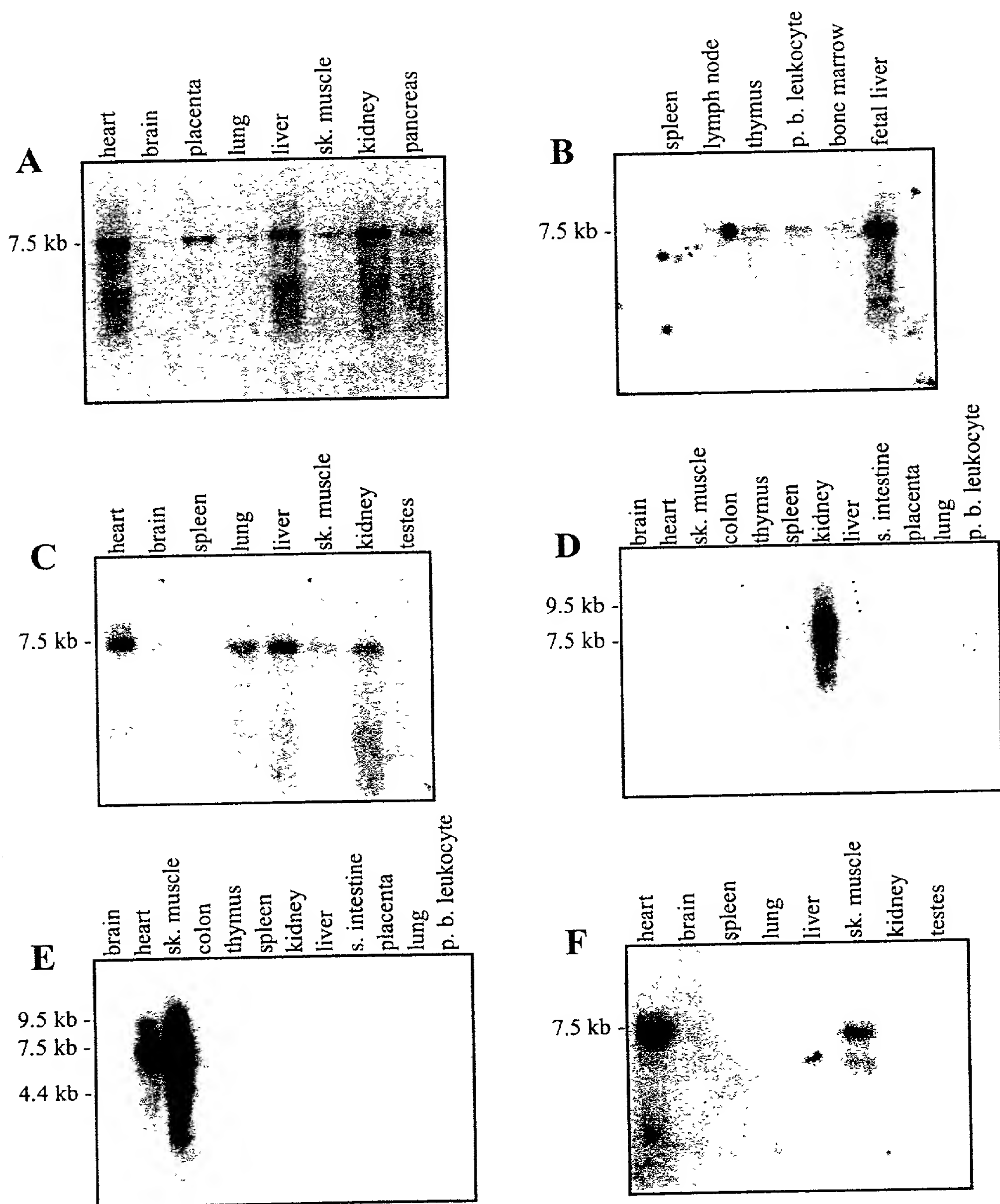


Figure 15

MK> 1 MSQKSWIESTLTRECVYIPSSNPHRCLPGCOICOOI MC XGRI (KCHCFTAL LA)
KK> 1 MSQKSWIESTLTRECVYIPSSNPHRCLPGCOICOOI MC XGRI (KCHCFTAL LA)
ME> 1

MK> 51 KYSDVFLGDHFNCAIFENSVEKHTEQSPILA VINFC S EYAKI KUDIRVH
KK> 51 SAAKQPS -----S-FCNSVEKHTEQSPITC TINFC S EYAKI KUDIRVH
ME> 1

MK> 121 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
KK> 121 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
ME> 15 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT

MK> 131 ANHVGDAK H S SRKICTIGIAPHGVIEL NOLVC DVAS TOTLHPLSKINHAK
KK> 174 ANHVGDAK H S SRKICTIGIAPHGVIEL NOLVC DVAS TOTLHPLSKINHAK
ME> 75 ANHVGDAK H S SRKICTIGIAPHGVIEL NOLVC DVAS TOTLHPLSKINHAK

MK> 241 HSHFILDGCTGVKYGAEV KRIEELK KCLIFAT TGAAT TGAAT
KK> 234 HSHFILDGCTGVKYGAEV KRIEELK KCLIFAT TGAAT TGAAT
ME> 115 HSHFILDGCTGVKYGAEV KRIEELK KCLIFAT TGAAT TGAAT

MK> 301 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 294 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 195 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 361 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
KK> 352 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
ME> 255 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT

MK> 421 DIANNE EYVGCQVVG
KK> 421 DIANNE EYVGCQVVG
ME> 315 DIANNE EYVGCQVVG

MK> 438 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
KK> 429 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
ME> 375 LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT

MK> 483 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 474 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 435 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 543 MNRRSGRNTSSST LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
KK> 533 MNRRSGRNTSSST LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT
ME> 494 MNRRSGRNTSSST LKLEWOMELPKLVISVHGC KFFE E KCLPKCLIFAT TGAAT TGAAT

MK> 603 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 580 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 523 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 663 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 639 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 583 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 723 KLAVERSLRPFVAHTCTOMEL DMMGRINMKKRS EYV EYV EYV
KK> 699 KLAVERSLRPFVAHTCTOMEL DMMGRINMKKRS EYV EYV EYV
ME> 643 KLAVERSLRPFVAHTCTOMEL DMMGRINMKKRS EYV EYV EYV

MK> 783 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 759 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 703 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 843 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 819 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 748 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 903 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 879 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 808 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 963 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 930 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 859 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1023 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 990 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 919 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1070 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1033 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 979 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1130 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1093 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1039 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1184 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1150 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1099 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1244 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1210 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1159 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1259 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1270 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1174 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1291 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1300 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1192 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1337 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1390 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1210 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1387 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1450 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1240 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1434 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1510 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1270 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1466 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1570 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1283 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1503 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1630 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1310 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1544 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1690 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1316 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1603 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1750 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1370 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1663 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1810 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1413 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1723 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1870 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1462 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1783 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1930 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> 1515 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

MK> 1843 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
KK> 1990 EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC
ME> EYLOHSPH PVVCEGTGRAADLLA LKLEWOMELPKLVISVHGC

Figure 16

MELANOMA_KINASE> 1 -----MSQKSWIEST
KIDNEY_KINASE> 1 -----MSQKSWIKGV
MELASTATIN> 1 -----
DmLTRPC1> 1 -----MYFETN
CeLTRPC1> 1 MNLGYRRHYASSPEVWCTMESDELGVTRYLQSKGGQVPTSTTTGGAGGDNVPTTSQAQATFNSGRQTGMSSGDRLNEDVSATANSALVLPPLFNQMFTESS
CeLTRPC2> 1 -----MDKRGSIIVPAHKVAESLRANSVTVEENESERETETQTKRR-----RKKQRTSSDKAPLHSAAPRVQKEDWKMHLADISGRKRGNSTTSHSGHATR
CeLTRPC3> 1 -----MRASRRVRKLVRRHASLIENIRHRTSSFLRLINAP-----RNSMCNANTVHSISSFRSDHLSRKSTHKFLDNPNLFAIELTEKLS-----
MTR1_LTRPC5_> 1 -----MQDVQGP RPSPGSPGDAEDR
LTRPC6> 1 -----
trpc7_LTRPC2_> 1 -----MEPSALRKAGSEQEEGFEGLPRRV

MELANOMA_KINASE> 11 LTKRECVYI FSSKDPKALPGCQICQQLVPCFCCVVKQACFTASLAMKYSVVKLG-----DHFNQAISSSPEKHTEQSPTWAYVNNQ
KIDNEY_KINASE> 11 FDKREGSTF PSSKNPRTTPVCQVQCNLIQYCCCLIGDAGLDYSWISAAGKE-----SSQSSPEKHITKSVNTETHIND
MELASTATIN> 1 -----MDSNPOCCQOFTNCHIFPLSAAPSNEEES-----KQVETQPKHSAVPHQTSYPTTSYVIEG
DmLTRPC1> 7 VWFHQPRSW ETNFQKKEIKFIPCPDDTCCGQAQITHTPIGIESGSPG-----CLLPTNTRPQPTTAYTTEP
CeLTRPC1> 111 NMSLNRRHWRETFTRFCSRFIASSDLHGGCTTRDARNIPELTSEFLQKRSVAALQORSISNVNDDINTONMYTKRGANKKTHITVSLADEFQVET
CeLTRPC2> 97 AGSLKGNWTECLKMKQSYFVPSQFSEBQCGHRSKTEEVLERQKNHPLNHLTPGHEVDTTDADADDNEVNLTGPR-----MSTQSHREIVPTAYVNVIE
CeLTRPC3> 80 -----PPWIENTFEKBEIRFAALPDPERCCGCPLSAATPASTFFS-----TLPVHLLKEQQTTHANNQTSTLNESTV
MTR1_LTRPC5_> 19 RELGLHR-----
LTRPC6> 1 -----
trpc7_LTRPC2_> 25 TDLGMVSNLARSNSLSFKSWRLQCPFGNNDQESLSSWIPENIKKKECVYFVSSKLSLDAGVVCQGYTHEQHLEFATKPHTFQGTQDPKIVQEMPTAFDVT

MELANOMA_KINASE> 100 ESSEYAKVPSMDIKKEVTCLEKKEQEPKLSVHGGQKEELHLEKQKGLKANVTICAWITTCVNTGVAKHYCALHASSER-----KICFSA
KIDNEY_KINASE> 93 GEHTHAKITTSHTKLDHCHIMKTKKEPKLSVHGGQONETPSKPEESQCLKAETTCAWITTCVNTGVAKHYCALHASSER-----KICFSA
MELASTATIN> 64 GGYSNAMVPSHTKEDSIHIMKTKKEPKLSVHGGQONETPSKPEESQCLKAETTCAWITTCVNTGVAKHYCALHASSER-----KICFSA
DmLTRPC1> 84 CAHPTIACVPRISDTRBELCLETNEMLEPKLTPVCKKANTLQAKLKEIRKGLKANVTICAWITTCVNTGVAKHYCALHASSER-----KICFSA
CeLTRPC1> 221 GHPYIAQVPRNIDIEAYTCLTEFVCHSHPLKLVHGGTSKPLDCLNTPRKLKAETTCAWITTCVNTGVAKHYCALHASSER-----KICFSA
CeLTRPC2> 204 -----TABULAFASLDERDHLHARVVKPKKLELHNGTTEKLOPKLARTPRKGLAKEDAWILLSEDEGVAKHDSALHCHENESK-----MHA
CeLTRPC3> 158 CAHPTIACVPRISDTRBELCLETNEMLEPKLTPVCKKANTLQAKLKEIRKGLKANVTICAWITTCVNTGVAKHYCALHASSER-----KICFSA
MTR1_LTRPC5_> 33 SGKPKKVPSPGVASVDFDIASHPAINATSVVEEQEPAKSWIRVLEKGLKAAJSTGAWITTSIRVAGHYCAVDSLSLSTKVTFVMS
LTRPC6> 1 -----MASTGGTTPMVA
trpc7_LTRPC2_> 135 -LSQVKKVVRVQDTPSSVYHLLTPQHGLDNLNLEWTSKNNKPLKLSSTFPGLEVEVQITGAWITTCVNTGVAKHYCALHASSER-----KICFSA

MELANOMA_KINASE> 207 WGVLENPNLIG--EVVAPQCLLNL-SKLVNNDLHSHFLVLGGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
KIDNEY_KINASE> 199 WGVLENQRLIG--EVVCLVCLDNL-SALTINSMSHFIISLGGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
MELASTATIN> 171 WGVLENQRLIG--EVVTRVCLDNL-SKLVNNDLHSHFLVLGGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
DmLTRPC1> 191 WGVLENQRLIG--EVVPCPSISSER-SKLVNNDLHSHFLVLGGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
CeLTRPC1> 328 WGVLENQRLIG--EVVTPPTPSSSK--GFTGLNHRASYLVDNGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
CeLTRPC2> 310 WGVLENQRLIG--EVVSTVTIANVFNNTKELNDNHEYSFSGNGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
CeLTRPC3> 267 WGVLENQRLIG--EVVHYVDVHSLSVNANVIGLHNRHGYELDNGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
MTR1_LTRPC5_> 142 LGRNLDHRIEEAEQEFVHHPPEDDGGSGGPHCS--SNLSHPLVLP--PPKGGDLTEALRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
LTRPC6> 17 WGVLENQRLIG--EVVTPPTPSSSK--GFTGLNHRASYLVDNGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV
trpc7_LTRPC2_> 244 WGVLENQRLIG--EVVTPPTPSSSK--GFTGLNHRASYLVDNGTVGKYGALVFLRELENTINQFIHARIGQGVVVALEEGGNVILTLELQESPVV

MELANOMA_KINASE> 314 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
KIDNEY_KINASE> 304 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
MELASTATIN> 278 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
DmLTRPC1> 298 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
CeLTRPC1> 434 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
CeLTRPC2> 412 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
CeLTRPC3> 372 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
MTR1_LTRPC5_> 252 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
LTRPC6> 126 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF
trpc7_LTRPC2_> 352 VCGGCGRAADLAATHQTEFGCN--EPDAEPDSTIKTHNGQNEALHQTLECKKRAHVPFQCS-----HQHVAITLALKCT-----AATF

MELANOMA_KINASE> 415 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
KIDNEY_KINASE> 405 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
MELASTATIN> 379 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
DmLTRPC1> 404 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
CeLTRPC1> 535 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
CeLTRPC2> 515 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
CeLTRPC3> 471 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
MTR1_LTRPC5_> 356 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
LTRPC6> 227 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH
trpc7_LTRPC2_> 460 IAWNRVDIARSHHPTVYQOOLVG-----SFGAMDAIMMREVEFVETIRKSH

MELANOMA_KINASE> 467 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
KIDNEY_KINASE> 457 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
MELASTATIN> 489 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
DmLTRPC1> 456 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
CeLTRPC1> 587 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
CeLTRPC2> 567 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
CeLTRPC3> 523 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
MTR1_LTRPC5_> 408 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
LTRPC6> 279 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S
trpc7_LTRPC2_> 512 FELTIRLEELYNKQSPKPMIFHARDKQGNIPPCVTHIDIGLVHYLGGTVFCTYTPRFFFLYN-----SLGNNRRSGRNTS-----S

MELANOMA_KINASE> 554 STPQLRKSHSEFNRRADKKEKMRHNFHTAQPYRPKIDTVMEEG-----KKKRTKDEIYDIDDPETKREPTLNSILWACM
KIDNEY_KINASE> 533 ---KYKHQRHSSGNRNESAESTLHQFHTAQPYRKFEKSVLHK-----SRKKSKEQNSDD--PESTGLNLLNLLMAM
MELASTATIN> 564 -----PKRKPAKILKLEDEDEPPAKGKKK-----KKKKEEIDVDVDPVSRQCPHSEMYAVIM
DmLTRPC1> 534 -----ACRKSSTYQYQYAGANS--SLVTLPLPTSEMALFE-----FPNELLVSGFRHNTSPSCSTSRLLFEKWAHTM
CeLTRPC1> 694 GVGGSVSVAGVFNSEFGNQPPLDPHNSLSGSRALSNIHLWSAFRGNFPANPMRPNLGDSDRGSEFDELSLTSASDGSQTEPDRTYSEIMWAVIT
CeLTRPC2> 647 SNGGRNDVIGPSQDAGRERMSMQISLNNRNSIISLFGGGGX-----RESDDDDPSNTEEEANMFTPTPTSDIMWAVIT
CeLTRPC3> 601 -----SYFHRKRKIVQKELF-----KSDDDNDNEEDDFSANENULLWAVITSHG
MTR1_LTRPC5_> 488 -----CDRR--AEKGPAPK-----TGQWLLDLNQSSENPRLFLAVIQNH
LTRPC6> 351 -----WDPHFGQGFGESEMYLSD-----KATSPSLDAGLGQALSLULWAVITSHG
trpc7_LTRPC2_> 583 -----NDRLRLLLPVPHVKINVOVSLR-----SLYKRSSGHVFTTMDTIRDLWAVITSHG

MELANOMA_KINASE> 638 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
KIDNEY_KINASE> 613 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
MELASTATIN> 628 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
DmLTRPC1> 609 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
CeLTRPC1> 804 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
CeLTRPC2> 733 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
CeLTRPC3> 653 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
MTR1_LTRPC5_> 534 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
LTRPC6> 401 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS
trpc7_LTRPC2_> 638 ARLWQHGEESMAKALVACLYSSELYFANSDIVDTSEETKQSNHGOALDILQSEPCHEIMAKLLIYELHWSNCTCLAVSRLIYVATITNIS

MELANOMA_KINASE> 748 MRLNMKSWYKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
KIDNEY_KINASE> 723 MRLNMKSWYKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
MELASTATIN> 738 MRLNMKSWYKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
DmLTRPC1> 719 MRLNMKSWYKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
CeLTRPC1> 914 HGLNMTHSNKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
CeLTRPC2> 843 QGGLNMTHSNKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
CeLTRPC3> 763 HGLNMTHSNKVLSTVPAILLVYKAEYSHIFQDARQMTM--DSENNEFNITEEIPMEVFVIRILSNEGKNEIOMK
MTR1_LTRPC5_> 638 WDCVAGTP--LWVTCGAFICAIYTNLITFSEAPLRTGLEDLQDLSDTEKSPLYGLQSEELVAPRAQCGRGP
LTRPC6> 507 WDCVAGTP--LWVTCGAFICAIYTNLITFSEAPLRTGLEDLQDLSDTEKSPLYGLQSEELVAPRAQCGRGP
trpc7_LTRPC2_> 744 WDCVAGTP--LWVTCGAFICAIYTNLITFSEAPLRTGLEDLQDLSDTEKSPLYGLQSEELVAPRAQCGRGP

Figure 17A


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MELANOMA_KINASE> 836 -----SKKIPPTTAVAFYHAPVVKFWFAYLFLLLTVALVQMEQL-----SVQEWIAYIYFTYAEKQ-----ETENSEAGKVMQIKW
KIDNEY_KINASE> 811 -----HCHLPWTAVAFYHAPVVKFWFAYLAFLLFTYTLVLMQFQF-----SVQEWISIVIFTNAPWR-----ECISEPGRITQVKW
MELASTATIN> 811 -----QRSHPDGTIGCEYNAPVVKFWFAYLFLLLNLVVLVRMDGWF-----SLQEWISIVYVLLAEKQ-----EELMPPGALISQTKW
DnLTRPC1> 808 -----HQPIREKMAEFYAPITKFWADSAAYFFLMEATLVKMEQME-----RWQEWYSIAVITLTAEKQ-----ETENSEPVAITLFSW
CeLTRPC1> 1114 DRPNPMEQFQGTRKPKKRRLEEFYAPITKFWFAYLFLFTFTFTVLLKTPERE-----VIEQWIAAYAAFLAEKQ-----KIMSLAKPFYEIRTY
CeLTRPC2> 1063 SSRNVTQVQYTQPPISWKIMIEFYKAPITTTALFFAEMFLILLTNLVKTKORIA-----SWSEMYIAYIVVWTAEIGK-----VVESTIADTSKPVLKQLRF
CeLTRPC3> 863 YGSASSMMFKREPQLNKFERAFYSPITKFWSCALIFITTONCILLTSLKE-----SKYEWITINTVTLISGHAP-----KATSEGGSRINEVKWF
MTR1_LTRPC5_> 717 -----AFELTRNRKEAGAPVSLGNVMEFSLFLFTYVLLVFRPPQGGSPGEVNTAFATLVLMEIRQGGFFT-----DFTDHLVKFTLY
LTRPC6> 591 -----GRCRLRHFAGAPVTIEMGNVLYLFLFLFERNVLLVFFQFAR-----PGSLLEHAFATLLCBEMRQGLSGGGSLASGGPGGHASISQRLRL
trpc7_LTRPC2_> 785 -----AARARATAPVVEHLNIDYEFELCLFERNVLYFFQFAR-----SWCECALMLHESILVCEMRQLFYD-----PDECCIMKAAFL

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MELANOMA_KINASE> 920 FSPENLISSTLAIISFEKCGIGFEQAKWNFANAYDNHVFVAGRIYICNIIEMVRLDLFLAVNQAGPYITKICKTANFMYIVVDAIVLLSPGVGPKKAIY:----H
KIDNEY_KINASE> 895 FSPENLITZTAIGLESAGVIRWGDPP-----FHTAGRRIYCNIIEMVRLDLFLAVNQAGPYITKICKTANFMYIVVDAIVLLSPGVGPKKAIIS:---K
MELASTATIN> 895 FSPENLITZTAIGLESAGVIRWGDPP-----FHTAGRRIYCNIIEMVRLDLFLAVNQAGPYITKICKTANFMYIVVDAIVLLSPGVGPKKAIIS:---E
DmLTRPC1> 892 AWMNMPNPGGAATLFLVGLAFEFRENT-----MDIGRVIVCYVSIWZLPALNVLGNKYLGLPLTWKQKQKNMIFVLLVWLMRSGVSPDAIY:---N
CeLTRPC1> 1209 VCSFENVCVTALIEFVGVFVSCFG-----SVAYSRVILACFSVMTLLLYMSVHPKELGPYITAKCKQNSHIVLVVTLSPFLAR:SIY:---D
CeLTRPC2> 1162 FFOVRUGLLAFVCTTGVVRIISPT-----TKTLGRFIIHISVTSRLNLYLSVQGLGPYINVAEPLTIPLCVNFITLYAGLL:SIY:---Y
CeLTRPC3> 958 YAKLNIIWTSAPLFEKCGEGLVSMY-----RKSQGRVLSFSNVIQVLTLYLSVRPLLGPYITQAKQKWSQCHICLLLELMALGNELALTE:--V
MTR1_LTRPC5_> 803 VGSNNRKNCVVAIFLFRVTCVLLPSA-----FEAGRTYLDVPEVETRLRHIEHNNHGLPKIVVERAKDVEFTQFTSYWLVAYVTT:LLHHDGRSL
LTRPC6> 866 FASQWDQCDNAITCTALVGCGLTEGL-----YHLGTYLQLEMTVRLRHIEHNNHGLPKIVVERAKDVEFTQFTSYWLVAYVTT:LLHHDGRSL
Ltrpc7_LTRPC2 > 864 FASQWNKILVGAIFLFAVLGTLISLAT-----LYGSRVTSDFILQVRLRHIEHNNHGLPKIVVERAKDVEFTQFTSYWLVAYVTT:LLHHDGRSL

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MELANOMA_KINASE> 1026 EAPSWTAR---DIVF-----EYWHITGEVYRGEIV-
KIDNEY_KINASE> 992 EPPSWSLAP---DIVF-----EPWHTYGEVYRAGNIV-
MELASTATIN> 992 EKPSMKAR---NIFY-----MFWHTYGEVFAQQITLY-
DmLTRPC1> 988 KQPTWSEIK---EVIAGSITAPGFLGALGHNTRSSYHRGYHTMGAPPVTTTAASTTTGSSSTVPAATTSTTAPIHNEHSNLTSGNLTNVTFQPPHLYGEVEAGQIPP-
CeLTRPC1> 1304 ETWHNIVRNIFL-----KRYEILYGEVYAGHTIT-
CeLTRPC2> 1258 EDWHNIVRNIFL-----QRYEILYGEVYASITIT-
CeLTRPC3> 1056 KDWHNIVRNIFY-----KRYEILYGEVYAGHTIT-
MTR1_LTRPC5_> 903 EWIFRR-----VLYRPLQFQIPLDEIEA-
LTRPC6> 786 ESILFR-----VFYRPLQFQIPQEDMVA-
trpc7_LTRPC2_> 964 ENLFRG-----AVYSLTFTQIPG-YLGV-

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MELANOMA_KINASE> 1057  S-----VIPTQGGPTNLTPFLQAVLFWQYITNLLLEAFNNMLQKATENIWKDRYHFTMAHHKEVLDPPPLDLSHTVSFCCICK
KIDNEY_KINASE> 1023  S-----SQSPQPPCSLTPLFLQAVLFWQYITNLLLEAFNNMLDLESNNLWKNRYRYIMTYHLEPWCEPPLDLSHMLTFRALCC
MELASTATIN> 1023  RVVINPPCGEN----LYDEEGKRLPFCPCAMTEALACLVVANILLNLLAEVNNITFEFKSISNQWKPQRYLTATEFTLVPPPMILSHYVITNRLSG
DmLTRPC1> 1094  CGED-----PSQPGCTGHTTPTITSLVLLANILLNLLAEFNNITENEVNSVSHVWFORITMEYQQFVLPPPTALCGVYILQVYVR
CeLTRPC1> 1335  DEADWDQHLENG---GVVILNGTGLSCPCYWWPLLTFTLLANILLNLLAEFNNITENEDVQLPQRYKQMEYSTFLPPPLTPYGYVILQVVR
CeLTRPC2> 1289  EDIWOQTHEDEN---IPISMLN-VGHETPCYWWAPGQITLATHNLLNLLAEFNNITENEGCTYFEKHQSRETLFERYGOQMEYSTWLPPPTILYVIVFNLIKS
CeLTRPC3> 1087  SDGIR-----CFQCYIEPPLVVLVIVANILLNLLAEFNNITENESIEKSKELPQRYQQMEYHNSFLPPPTSHLAVYHFDQYZYN
MTR1 LTRPCS_> 930  RYN---CSTHP---LLEDSP-----SCPSYNNMLVLLVTLVLLVTLNLLNLLAMFSYTFQVQGNEDMFQKRFQYNNITVEYHFTAAAPPLDLSHTSTIRRFK
LTRPC6> 813  LMHSNCSSEP---GFWAHPGGAAGTCVSQYNNMLVLLVTLVLLVTLNLLNLLAMFSYTFGKQGNSDLYNKRQRYIRLRHSFAAPPSVITIRRLRQLR
trpc7 LTRPC2 > 990  NFNPEHCSPNGTDPYKPKCPESDAQCVQPAFEWLVLLGLVLLTNNILLNLLAEFNNITENEGHEDLVKQFQHDILHEHYHCSAAAPPSILSLHQFIMRAVL

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MELANOMA_KINASE> 1148 ----KKKDDTSDG---PKLFLIEDLQKLHDFECCVEMFNEKDKFHSGSEERIVVFERVQCICQKNGRVN-YKRSQSLSLQIGHLODLALTDTLKT
KIDNEY_KINASE> 1110 ----TRAPHDQEGVGLKIKLKKNTKLHDFECCVERKFFEMEDVNGCBERIVFSERVTEMFYOLKKNKVS-FKKSHLSLSQVGHLODLALTDTLRV
MELASTATIN> 1127 G---CRGREGQDERRGKLLKFLDDEGALHDFECCVCHFFKIDEQQSSEPIVFSERVNNMSLEENERET-FMYSQTVIDFLALEELNRMMNAGEN
DmLTRPC1> 1185 ----KAKGLEVRQNGKLKLEKMLERLYDFEEVCEGFFHQQIILNQLDLPVNNFVETVTSQKEDENQEN-MGTATQNLHFRLRKEESLEQLSHAV
CeLTRPC1> 1442 RLSCSGOERNPILLKIAELFDNNDKLNHDFECCEDLAEALNKEKNTSNEPIRLADIFITCLNKLIDQAKES-IGQVDNDLEERLSVEKAQNEITCEVRA
CeLTRPC2> 1395 ----SSMFEEKNLFGQSLKLFLEPDEEVTFEESDEVMKSFTEKKNLSENDEPIHREMEPTAHLNLSHSHUTOLEF-TLFEEDRELEHMKNDSRHKEQNLNLD
CeLTRPC3> 1175 ----LSPDTRFRSRHSKLSLDELEHRCDFEEDLITLTTHIR---KLKLNTEPLSVHLLTLTCQVNDHMQENF-LNSRYVDLETKIDHSNSDEVQIKN
MTR1 LTRPC5_> 1030 ----EAHKK---EHLERDPPDLQDVTFTVQKCNLSMKCKRRRDSEGVIRKIANVDFIAKYLGGIRFY-----EKRKQKLSQNYCSVIVSSMDVIAQ
LTRPC6> 921 G---PSPQSPSPALEHFMKPKAEKLTLSVSHKENALLAKARDKREDSERIER-SQKVDLAKQLGHRFY-----EQRLKVLAREVQCSRVLGWVT---
trpc7 LTRPC2 > 1100 K---TPAKRI---KCLNNKEKNELAALLSYLYKLNQNLQNGFQQRQRPSEITEDSNVLANVDLDDLPKRSVGEQRLASLGEQVQTAQALHWTARTIRA

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MELANOMA_KINASE> 1249 -----LTAQKASEASKVHEITELSIKHUAQNMIDD
KIDNEY_KINASE> 1214 LSAVDTLQEDEALLAKRAHSTCKKLPHSWSNVICAEVLGSMETAGEKKYQYSSMPSSLRLSLAGGRHPPRVORGALLEITTSEREAATNVEIQEQVIOIIVVSGVSPN

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MELANOMA_KINASE> 1282 G-----GVRPSVWKKKHGVNTLSSSLP*CDLESNNPFCNICILMIDK*SCQNT*FG-----EDLEAPPKRKEFNFPPEAGS*SSA
KIDNEY_KINASE> 1324 ROAHSKYGOFLVPSNLKRVPSAKTVLPLSRFEVDVLAIEDDQTEVLVHLNGTPVVDVDSASVDEPKKKE*TAHLDGQDKAEVLPDLSCTPPRMTMSSPL*QAK

MELANOMA_KINASE> 1355 **Y**PPF-----**Y**-----AV**Y**PPPL**Y**GLHGV**Y**L**Y**FI**Y**FN**Y**KN**Y**Q**Y**KL**Y**GS**Y**SS**Y**SP**Y**HL**Y**SS**Y**PT**Y**K**Y**ST**Y**PS--**Y**CS**Y**RS**Y**LETGT**Y**IQ--ET**Y**V
KINSEY_KINASE> 1434 **Y**MO**Y**GG**Y**Y**Y**V**Y**NA**Y**F**Y**SE**Y**GE**Y**T**Y**GF**Y**SI**Y**KK**Y**W**Y**OT**Y**CL**Y**PT**Y**CD**Y**SD**Y**SR**Y**SE**Y**Q**Y**AO**Y**DS**Y**SD**Y**NT**Y**SA**Y**QS**Y**EC**Y**EL**Y**GP**Y**WL**Y**Q**Y**NS**Y**SL**Y**NP**Y**L**Y**RR**Y**Y**Y**FA**Y**HS**Y**SR**Y**PH**Y**SE**Y**KL**Y**MK**Y**I

MELANOMA_KINASE> 1427 SKATEGDNISECAFVGHDSMDLQPFEESEN-----KIKLLENNTSEN-----TKKVESLIGFTDCHRTSIPVHSKEKLSRRPSTEDL
KINSEY_KINASE> 1544 KIKNLGSGTGTGGAWAKKNTKDRSLKKKKNTGGLQPLTAVACGSDQLNBERGNSISFEFYSKNWFSSEFHTVEFYLIKMKMTKRGICCAIISDYLKOS

MELANOMA KINASE> 1508 HEVDSKRAALIPVWLQDRPSNREIPSEETNGHISPFKPMATNYYYSAFERNMLRLSCSIPTFPVPPRE-EPYTVYRLESSENIANNSSSWSLLEPKKEELKRL
KINEX KINASE> 1655 QDGLGNSLWDSPSTLNRLNLSIKKSTGINKKASTGSPDHHVYSLERNMLRLSCSIPTFPVPPRE-EPYTVYRLESSENIANNSSSWSLLEPKKEELKRL

MELANOMA KINASE> 1617 EMGGGLR¹⁶¹⁷ATVQCTWSEHOLIRSH¹⁶²⁴IPKSFLEPVVNTSS¹⁶³¹AKED¹⁶³²TVLHLCLREIQ¹⁶³⁹QRAAQKLTAENQ¹⁶⁴⁶KKK¹⁶⁴⁷IPYS¹⁶⁴⁸PRFLELVFLYCHSAG¹⁶⁵⁵TFAVECHTQGS¹⁶⁶²
KINEX KINASE> 1264 EMGGGIR¹²⁶⁴ATVQCTWSEHOLIRSH¹²⁷¹IPKSFLEPVVNTSS¹²⁷⁸AKED¹²⁷⁹TVLHLCLREIQ¹²⁸⁶QRAAQKLTAENQ¹²⁹³KKK¹²⁹⁴IPYS¹²⁹⁵PRFLELVFLYCHSAG¹³⁰²TFAVECHTQGS¹³⁰⁹

MELANOMA KINASE> 1727 HKYNNNNNGDELLPTNTLEE MLAFSHWTYYEYTRGELLVLDLQGVGENLTDFSVTKAEERFSCDNYFGPANLGEDAIINERAKHHHCNSCCRALKLPTRKRNDYTIIDK IFP
KINASE KINASE> 1030 KKYNNNNNGDELLPTNTLEE MLAFSHWTYYEYTRGELLVLDLQGVGENLTDFSVTKAEERFSCDNYFGPANLGEDAIINERAKHHHCNSCCRALKLPTRKRNDYTIIDK IFP

MELANOMA_KINASE> 1837 QDEPSDINLQPGNSTKDEESTNSVRLML-

Figure 17B

601-1-098CIP

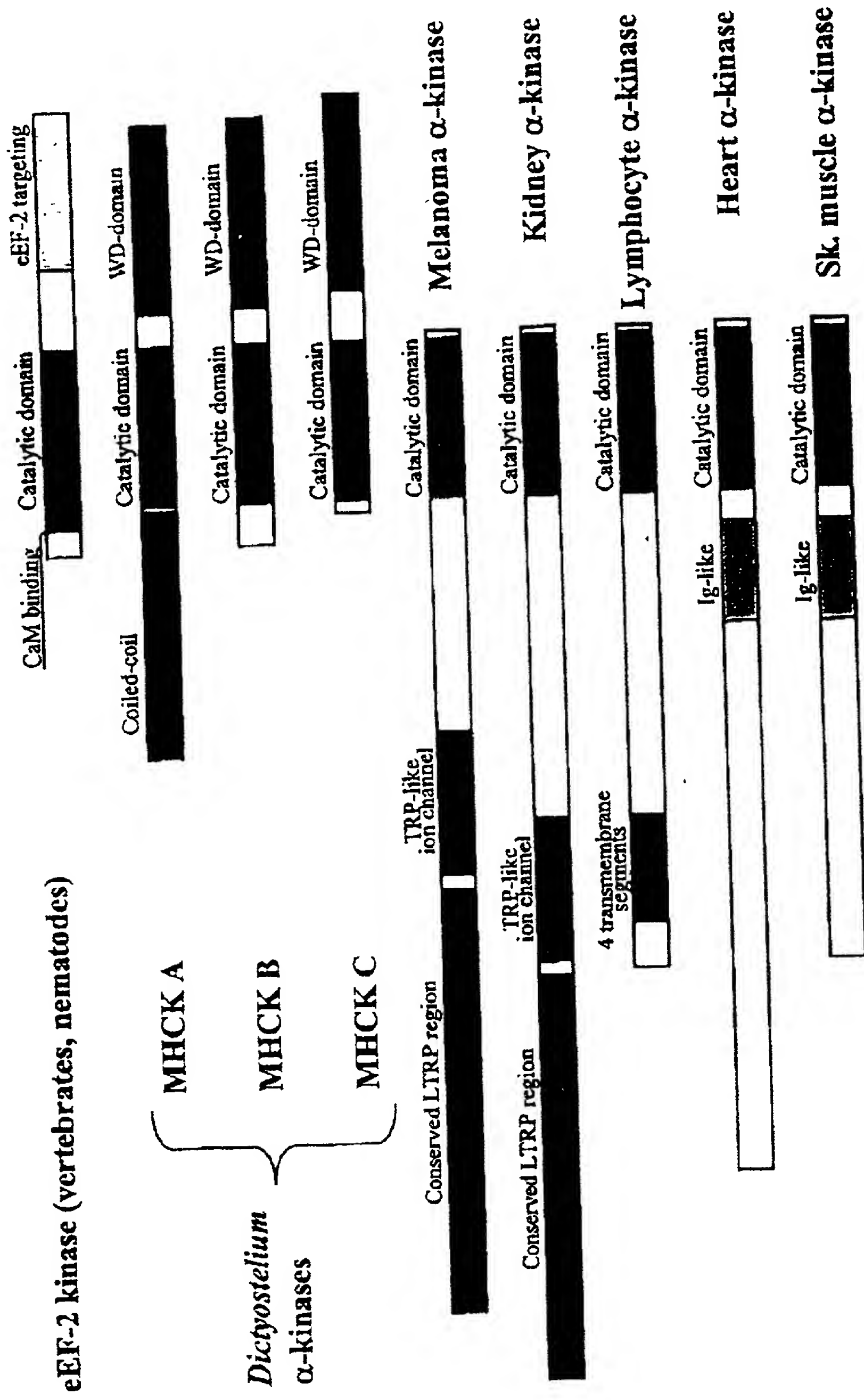


Figure 18

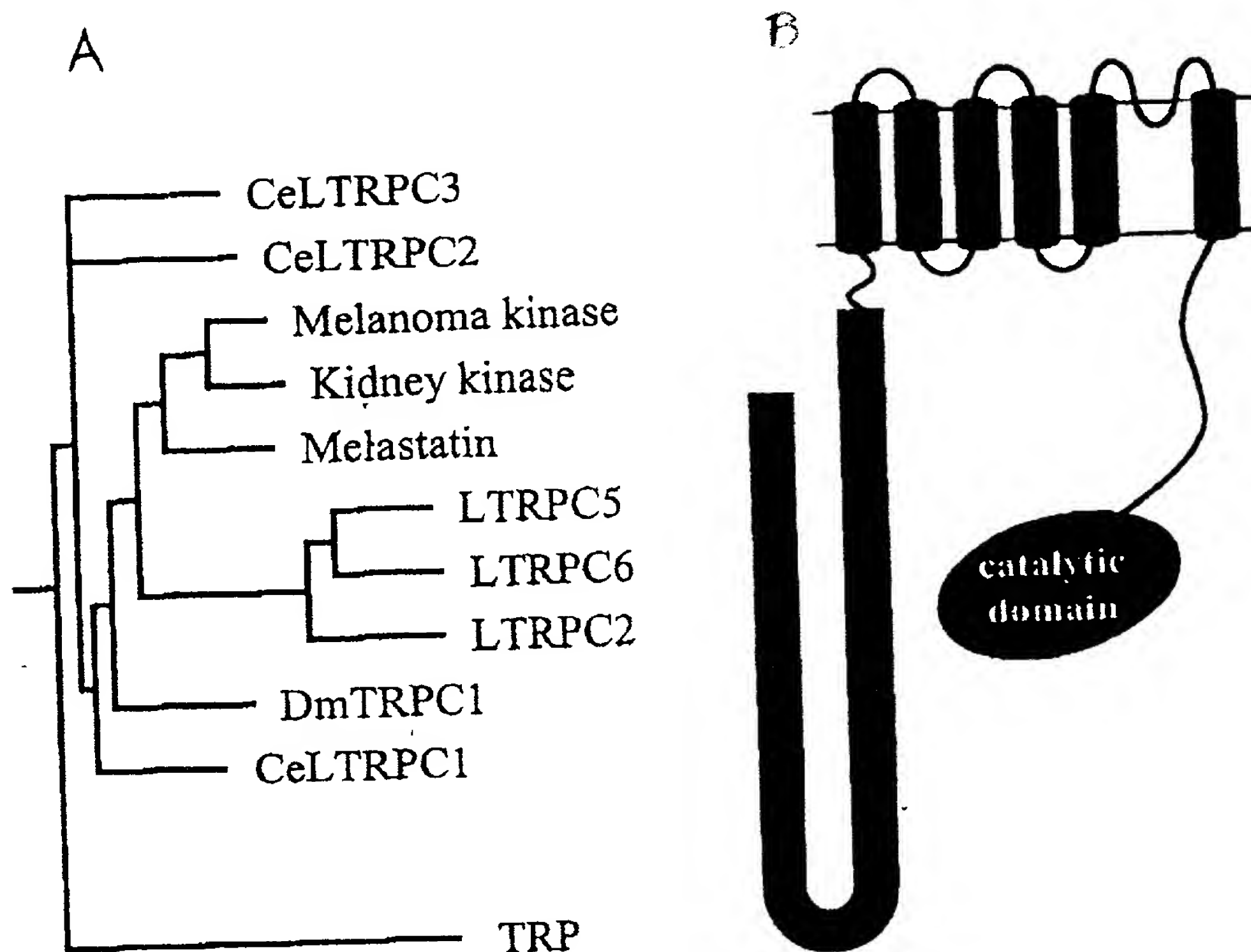


Figure 19